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Title:
Perfect score:
                                                                                                                                        OM protein - protein search, using sw model
US-10-041-006-7
1571
                                                              August 13, 2002, 08:55:18; Search time 17.52 Seconds (without alignments) 1590.520 Million cell updates/sec
                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence:

1 MRRPAAVPLLLLCEGSQRA.....WIHRIIPKLQEQPARLGGQK 290

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

ched: 283138 seqs, 96089334 residues

I number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : pIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID  618.5 39.4 343 1 A57014 prostas 594 37.8 270 2 S56160 mast ce 588.5 37.5 275 2 B35863 tryptas 581.3 7.0 274 2 A45754 582.5 36.0 274 2 A45754 583.5 36.0 274 2 A47246 580.5 35.7 275 2 A38654 580.5 35.7 276 2 A38654 580.5 35.7 275 2 A32410 580.5 35.7 275 2 A32410 580.5 33.9 638 1 KQHUP 580.8 33.9 638 1 KQHVP 580.8 33.0	Score Match Length DB ID Description	.5 39.4 343 1 A57014 prostasin (	565.5 36.0 274 2 JC4171 tryptase (	564 35.9 276 2 A38654 mast cell	560.5 35.7 275 2 A32410 tryptase (	533 33.9 638 1 KQHUP plasma	526 33.5 810 2 B30848 plasmin	518 33.0 638 1 KQMSPL plasma	517.5 32.9 417 1 S00845 hepsin (EC	517 32.9 638 1 KQRTPL plasma kal	513.5 32.7 237 2 S68702 tryptase (	509 32.4 455 2 A61545 plasmin (	505.5 32.2 416 1 S33777 hepsin (F	502 32.0 810 1 PLHU plasmin (	496.5 31.6 812 1 PLBO plasmin (	493 31.4 269 2 B32410 mastocy	491.5 31.3 1034 1 A53663	487.5 31.0 625 1 KFHU1 coagulati	479.5 30.5 812 1 PLMS plasmin (	479 30.5 790 1 PLPG plasmin (		478 30.4 460 2 B61545 Prasmin (	478 30.4 460 2 B61545 477.5 30.4 1420 2 A32869	478 30.4 460 2 B6.1545 plasmin (478.5 30.4 1420 2 A32869 apollipopi 469 29.9 1524 2 T30337 polyprott	SCO 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Quer Ouer 1009 1009 1009 1009 1009 1009 1009 100	Length 343 343 270 275 275 275 275 275 274 276 277 278 278 278 278 278 278 278 278 278	. אין רמממממממממרטררמררמררמררמרר פוררמרררמררר פו	A57014 S56160 B35863 A35863 A35863 A35863 A47746	prostasin (EC 3.4.2 tryptase (EC
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trypsin (EC 3.4.21	serine proteinease	acrosin (EC 3.4.21	acrosin (EC 3.4.21	chymotrypsin (EC 3	testicular serine	chymotrypsin (EC 3	oviductin (EC 3.4.	chymotrypsin (EC 3	acrosin (EC 3.4.21		. ~	enteropeptidase (E	tow-density tipopr	memorane cype-seri	membrane-bound arg

# ALIGNMENTS

Qy 6 AVPLLLLLCFGSQRAKAATACG-RPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCG 61	Query Match 39.4%; Score 618.5; DB 1; Length 343; Best Local Similarity 42.9%; Pred. No. 6.5e-47; Matches 124; Conservative 47; Mismatches 99; Indels 19; Gaps 7;	A57014 (EC 3.4.21) precursor - human prostasin (EC) 3.4.21) precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: A-May-1996 #sequence_revision 24-May-1996 #text_change 18-Jun-1999 C;Accession: A57014; A54866 R;Yu, J.X.; Chao, J.; Chao, J. J. Biol. Chem 270, 13483-13489, 1995 A;Title: Molecular cloning, tissue-specific expression, and cellular localization of A;Reference number: A57014; MUID:95286644 A;Recession: A57014 A;Status: translated from GB/EMBL/DDBJ A;Accession: A57014 A;Status: translated from GB/EMBL/DDBJ A;Accession: A57014 A;Residues: 1-343 CRES> A;Residues: 1-343 CRES> A;Residues: 1-343 CRES> A;Reperimental source: prostate A;ACcess: references: GB:L41351; NID:9862304; PIDN:AAC41759.1; PID:9862305 A;Residues: 1-343 CRES> A;Cross: references: GB:L43351; NID:9862304; PIDN:AAC41759.1; PID:9862305 A;Residues: A54866 A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification A;Residues: 45-64 CVIA> C;Genetics: C;Genetics: A;Genetics: GB:PRSGB A;Genetics: GB:PRSGB A;Genetics: GB:PRSGB A;Genetics: GB:S76446; OMIN:600823 A;Map position: 16p11,2-16p11.2 C;Genetics: GB:Gf0446; OMIN:600823 A;Map position: Signal seguence #status predicted <chid- c;ry="" f;3-3-44,7domain:="" homology="" trypsin=""> C;Keywords: glycoproduct: prostasin heavy chain #status predicted <chid- c;ry="" f;3-3-34,7domain:="" homology="" trypsin=""> F;3-3-34,7Domain: trypsin homology C;RY&gt; F;3-159/Binding site: carbohydrate (Asn) (covalent) #status predicted F;85,134,238/Active site: His. Asp, Ser #status predicted F;85,134,238/Active site: His. Asp, Ser #status predicted F;85,134,238/Active Site: His. Asp, Ser #status predicted</chid-></chid->	

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R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pra;Reference number: A35863; MUID:90251647
                                A; Molecule type: mRNA; DNA
A; Residues: 1-275 < VAN>
                                                                                A; Reference number: A35863; A; Accession: B35863
                                                                                                                                                                                                                                                                   tryptase (EC 3.4.21.59) II precursor - human N_iAlternate names: tryptase beta
               A;Cross-references:
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A; Residues: 1-270 <MUR>
A; Residues: 1-270 <MUR>
A; Cross-references: EMBL: D31789; NID: g517122; PIDN: BAA06598.1; PID: g517123
C; Superfamily: trypsin; trypsin homology
F; 26-262/Domain: trypsin homology <TRY>
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Lle: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones A;Reference number: S56160; MUID:95366971
A;Status: preliminary
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                                                                                                                                                                                  ;Species: Homo sapiens (man)
;Species: Homo sapiens (man)
;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
;Accession: B35863; A37193; I59473
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 GADIALLELKNPVNISSHVHPVSLPPASETFPSGTLCWVTGWGNIDNDVSLPPPPPPLKEV 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 QVPVVENQLCDLKYHKGVYTGDNIHIVRDDMLCAG·NEG-HDSCQGDSGGPLVCKVNGTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLIHPQWVLTAAHCVGPTIADPNKVRVQLRKQYLYY---HDHLLAVSRIITHPTFYATQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPLESLM----HRSPLCQEWG------IVGGQEAPGNKWPWQVSLRANETYWRHFCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122;
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     GB:M33492; NID:g339982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 594; DB 2;
Pred. No. 7.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
PIDN:AAA36779.1; PID:g339983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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A; Molecule
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R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A;Reference number: A35863; MUID:90251647
                                                                                                                                                                                                                                  C:Species: Homo sapiens (man)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C:Accession: A35863; A60939; A39326
C:Accession: A35863; A60939; A39326
A; Accession: D35863
            A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
                                                    A; Molecule type: DNA
A; Residues: 1-275 < VAN>
                                                                                                               A; Accession: A35863
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                                                                                                                                                                                                                                                                                                                                              tryptase (EC 3.4.21.59) I precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-21/Domain: signal sequence **status predictéd <SIG>F;2-30/Domain: activation peptide **status predicted <ACT:F;31-275/Product: tryptase I **status predicted <AAT>F;31-267/Domain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 16pter-16qter
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Characterization of a tryptase mRNA expressed in A;Reference number: I59473; MUID:93166209
A;Accession: I59473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:125890; OMIM:191080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: TPS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-275 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:S55551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scand. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Blom, T.; Hellman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
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A; Residues: 1-275 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A37193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A37193; MUID: 90369005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 HPQWVLTAAHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 AEQWVLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNG---SHFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 588.5; DB 2
Pred. No. 2.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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R;Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, J. Leukoc. Biol. 47, 409-419, 1990
A;Title: Purification of tryptase from a human mast cell line.
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C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
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A;Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocytoch A;Reference number: A39326; MUID:87109258
A;Accession: A39326
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A;Residues: 31-38,'p',40-41,'X',43,'T',45-48,'X',50
A;Experimental source: mast cell
A;Note: 44-Gly was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-275 < VA2>
A; Cross-references: GB: M33491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A60939; MUID:90244210 A; Accession: A60939
                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) III precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Cpate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Jun-2001 C;Accession: C35863; A35863; A35863; A38993 R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990 A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr A;Reference number: A35863; MUID:90251647 A;Accession: C35863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Note: the first nine residues of this sequence are inferred from genomic DNA of trypta
                                                         A; Molecule type: DNA
A; Residues: 1-9 <VA2>
                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 9-275 <VAN>
                                                                                                                          A; Accession: A35863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trons: 21/1; 78/2; 177/1; 221/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 IMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 IALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 GVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 GVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 VALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 HPQWYLTAAHCYGPDYKDLAALRYQLREQHLYY---QDQLLPYSRIIVHPQFYTAQIGAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 AEQWYLTAAHCF-RNTSETSLYQYLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNG---SHFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 587.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.7e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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F;1-21/Domain: signal sequence #status predicted <SIG>F;22-30/Domain: activation peptide #status predicted <ACT:F;31-27/Product: tryptase I #status predicted <MAT>F;31-27/Domain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser #status predicted
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C;Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to GenBank, April 1990 A; Reference number: A38893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C;Accession: A45754; B37193
R;Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A;Title: Cloning and characterization of complementary DNA for human tryptase.
A;Reference number: A45754; MUID:90009311
A;Accession: A45754
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A; Residues: 9-131, 'K', 132-275 <VA3>
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A; Molecule type: mRNA
A; Residues: 1-274 <MIZ>
A; Cross-references: GB:M30038
A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-30/Domain: activation peptide #status predicted <ACT>
F;31-274/Product: tryptase I #status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M30038
R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a
A;Reference number: A37193; MUID:90369005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tryptase (EC 3.4.21.59) alpha precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B37193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 VALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 GVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 GVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 HPQWVLTAAHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEQWVLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSAD 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J () ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McNeil, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.; Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast A;Reference number: A47246; MUID:93087489
A;Accession: A47246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: nucleic acid
A; Residues: 1-273 <MCN>
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Best Local
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         237
                                                   244
                                                                                                                                                                       119 DIALLKLTNPVNISDYVHPVPLPPASETFPSGTLCWVTGWGNIDNGVNLPPPFPLKEVQV 178
                                                                                                                         184 PIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLYCLYGQSWLQ 243
                                                                                                                                                                                                                 124 DVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 LVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 FPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDMLCAG--NSQRDSCKGDSGGPLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 RILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 KVNGTWLQAGVVSWDEGCAQPNRPGIYTRVTYYLDWIHHYVPK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 FYIIQTGADIALLELEEPVNISSRVHTVMLPPASETFPPGMPCWVTGWGDVDNDEPLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 YQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWYTGWGSPSEEDLLPEP 175
                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                            9 LLLLLCFGSQRAKAATACGRPRMLNR-MVGGQDTQEGEWPWQVSIQRNGS---HFCGGSL 64
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                                                                               PIIENHLCDLKYHKGLITGDNVHIVRDDMLCAG-NEG-HDSCQGDSGGPLVCKVEDTWLQ 236
                                       AGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                   IAEQWVLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSA 123
                                                                                                                                                                                                                                                                                                                                                  LLLTLPLLSSLVHAAPG---PAMTREGIVGGQEAHGNKWPWQVSLRANDTYWMHFCGGSL 61
AGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPK 271
                                                                                                                                                                                                                                                              IHPQWVLTAAHCVGPDVADPNKVRVQLRKQYLYY---HDHLMTVSQIITHPDFYIVQDGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLALPYLASRAYAAPAPYQALQQAGIYGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEQWVLTAAHCFRNTSETSLYQVLLG-----ARQLVQPGPHAMY----ARVRQVESNDL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.8%; Score 578.5; DB 2; 45.5%; Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%;
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Pred. No. 1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:g200519
NCBIP:119746)
                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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δÃ 밁 ρ B Q 멍 δÃ 밁 Ş

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einase inhibitors.

C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell tryptase #status predicted <MAT>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,233/Active site: His, Asp, Ser #status predicted
F;131/Binding site: carbohydrate (Asn) (covalent) #status predicted
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999 C;Accession: A38654; B38654; D35646; I59478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-274 <IDE>
A; Cross-references: DDBJ; D
C; Comment: This enzyme is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tryptase (EC 3.4.21.59) precursor - rat
N;Alternate names: mast cell tryptase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Ide, H.: Itoh, H.: Tomita, M.: Murakumo, Y.: Kobayashi, T.: Maruyama, J. Biochem. 118, 210-215, 1995
A:Title: CDNA sequencing and expression of rat mast cell tryptase.
A:Reference number: JC4171; MUID:96015171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    176 QVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGMLCAG--NTRSDSCQGDSGGPLVCKVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 KLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQ 239
                                                                                                                                                                                                                                                                                 234 TWLQAGVVSWGEGCAEANRPGIYTRVTYYLDWIHRYVPQ 272
                                                                                                                                                                                                                                                                                                                                                  240 SWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 DGADIALLELEIPVNVSTHIHPISLPPASETFPSGTSCWVTGWGDIDSDEPLLP-PYPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HPQWVLTAAHCVGLHIKSPELFRVQLREQYL-----YYADQLLTVNRTVVHPHYYTVE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AEQWYLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYA----RVRQVESNPLYQGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LLLLLALSPLASLYHAAPCPVKQRVGIVGGREASESKWPWQVSLRFKFSFWMHFCGGSLI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGS---HFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGS-PSEEDLLPEPRILQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%; Score 565.5; DB 2;
43.7%; Pred. No. 2.4e-42;
43.7%; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    basically specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509 R;Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E. Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990 A;Title: Different mouse mast cell populations express various combinations of at lea A;Cross-references: GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 3 s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly A; Molecule type: mRNA A; Residues: 1-276 < RE2> R:Reymolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E. J. Biol. Chem. 266, 3847-3853, 1991 A;Title: Cloning of the CDNA and gene of mouse mast cell protease-6. Transcription by A;Reference number: A38654; MUID:91139682 A; Accession: B38654 A; Molecule type: DNA A; Residues: 1-276 < REY> A; Accession: A38654

RESULT JC4171

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Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural A;Reference number: A32410; MUID:89352460
A;Accession: A32410
A;Koclession: A32410
A;Kolecula type: mRNA
A;Residues: 1-275 <VANN
A;Residues: 1-275 <VANN
A;Cross-references: GB:M24664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: aignal sequence #status predicted <ACT>
F;21-25/Product: tryptase #status predicted <ACT>
F;31-25/Product: tryptase #status predicted <ACT>
F;31-27/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                        tryptase (EC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
C;Accession: A32410
R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
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A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and A;Reference number: 159478; MUID:94023807
A;Accession: 159478
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A;Accession: D35646
A;Molecule type: protein
A;Residues: 32-54 <RE3>
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A; Residues: 1-276 < RES>
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(words: hydrolase; serine proteinase; zymogen
(l/Domain: signal sequence #status predicted <SIG>
31/Domain: activation peptide #status predicted <ACT>
-276/Product: mast cell proteinase 6 #status experimental <MAT>
(32-268/Domain: trypsin homology <TRY>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 QPNKPGIYTRVTYYLDWIHRYVPE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YHTGLYTGDDFPIVHDGMLCAG--NTRRDSCQGDSGGPLVCKVKGTWLQAGVVSWGEGCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVGPHIKSPQLFRVQL-REQYLYYGDQLL--SLNRIVVHPHYYTAEGGADVALLELEVPV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATACGRPRMLNR---MVGGQDTQEGEWPWQVSIQ---RNGSHFCGGSLIAEQWVLTAAH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLVYSAPRPANQRVGIVGGHEASESKWPWQVSLRFKLNYWIHFCGGSLIHPQWVLTAAH 75
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Best Local
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                240 SWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                  KLAVPIIDTPKCNLLYSKDTEFGYOPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQ 239
                                                                                                                                                                      ASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQ 179
                                                                                                                                                                                                      IHPQWVLTAAHCVGP-----NVVCPEEIRVQLREQHLYYQDHLLPVNRIVMHPNYYTP 116
                                                                                                                                                                                                                                                                        PLYLALALLGSLYPYSPAPGQALQRYGIYGGREAPGSKWPWQYSLRLKGQYWRHICGGSL 63
                                                                                                                                                                                                                                                                                                        PLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGS---HFCGGSL 64
VWLQAGVVSWGEGCAQPNRPGIYTRVAYYLDWIHQYVPK 273
                                                                   QVKVPIVENSMCDVQYHLGLSTGDGVRIVREDMLCAG - - NSKSDSCQGDSGGPLVCRVRG
                                                                                                                                    ENGADIALLELEDPVNVSAHVQPVTLPPALQTFPTGTPCWVTGWGDVHSGTPLPPPFPLK 176
                                                                                                                                                                                                                                      IAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYAR-----VRQVESNPLYQGT 119
                                                                                                                                                                                                                                                                                                                                              116;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                            35.7%;
                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                            Score 560.5; DB 2
Pred. No. 6.5e-42;
                                                                                                                                                                                                                                                                                                                                              Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                              275;
                                                                                                                                                                                                                                                                                                                                              17;
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Search completed: August 13, 2002, 08:57:23 Job time: 125 sec

GenCore version Copyright (c) 1993 - 2000

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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US-09-088-551-2
US-08-944-483-66
US-08-978-4048-6
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US-08-944-483-63
US-08-948-219-1
US-08-681-151-3
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US-08-681-350-1
US-08-750-711-1
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Sequence	8-892-544-4	N	230	30.8	483.5	42
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Sequence	US-08-469-486-54	۳	790	'n	502	28

54, Appl 1, Appl 1, Appl 1, Appl 1, Appl 2, Appl 2, Appl 1, 2, Appl 47, Appl

ALIGNMENTS

RESULT 1 US-09-088-651-2 US-09-088-651-2 Sequence 2, Application US/09088651 Patent No. 6165771 TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear GENERAL INFORMATION:
APPLICANT: CUINKENBEARD, HELEN E.
APPLICANT: SOUTHAN, CHRISTOPHER D.
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6 FILING DATE: JUNE 1, 1998
FILING DATE: JUNE 1, 1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: GB9712088.5
FILING DATE: 10-JUNE-1997
APPLICATION NUMBER: GB97308295.1
FILING DATE: 17-OCT-1997
APPLICATION NUMBER: GB 9803650.2
FILING DATE: 17-OCT-1997
APPLICATION NUMBER: GB 9803650.2
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: GH30358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEPAX: 611-407-0701 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,651 CORRESPONDENCE ADDRESS: MOLECULE TYPE: ADDRESSEE: RATNER & PRESTIA STREET: P.O. BOX 980 CITY: VALLEY FORGE STATE: PA COUNTRY: U ZIP: 19482 USA UMBER: US/09/088,651 JUNE 1, 1998

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US-08-944-483-66
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                                   INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                    SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
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                                                                                                                                   NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
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                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                       TELEX:
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ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                APPLICATION NUMBER: 60/0 FILING DATE: 04-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.C. COUNTRY: 02210-2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: WO
STREET: 600 A
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 VCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 GMNCWVTGWG--SPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDM 212
                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 QSKVTELQPRVVPQTQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 H-----RIIPKLQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 LCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GLHCTVTGWGHVAPSVSLLTPKP--LQQLEVPLISRETCNCLYNIDAK-PEEPHFVQEDM 177
TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 25-NO
                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                  TELEFAX:
                                                                                                                                                                                                                NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 LVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFET 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LDSYSEDAKVSTLKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 MYGGQDTQEGEWPWQYSIQRNGSHFCGGSLIAEQWYLTAAHCFRNTSETSLYQYLLGARQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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              amino acid
                               270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Atlantic Avenue
                                                                                                                  617-720-2441
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VENTION: MAST CELL PROTEASE THAT CLEAVES
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                                                                                                                                                                                           36,637
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Pred. No. 1.2e-58;
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                                                                                                                   INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 GADIALLELKNPVNISSHVHPVSLPPASETFPSGTLCWVTGWGNIDNDVSLPPPFPLKEV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                              TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 QVPVVENQLCDLKYHKGVYTGDNIHIVRDDMLCAG-NEG-HDSCQGDSGGPLVCKVNGTW 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKL 181
TOPOLOGY: 1.
                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 LQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOY-97
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                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 80801/7090
                                                                                                                                                                                                                                     NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                     STRANDEDNESS:
                                                                                                                                                         TELEFAX: 617-720-2441
                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPLESLM----HRSPLCQEWG-----IVGGQEAPGNKWPWQVSLRANETYWRHFCGG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                  linear
  No. 5968782e
                                     single
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44.0%; Pred. No. 9.1e-58;
ative 48; Mismatches 87; Indels
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MAST CELL PROTEASE THAT CLEAVES
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US-08-978-404B-6
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US-09-016-366A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stevens, Ric
APPLICANT: Huang, Chifu
                                                                                                                                                                         NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REGISTRATION NUMBER: B01 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 05-FEB-1997
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                                                                                                                                                                                                                                                                         FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLYGQSWLQA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 IALLKLTNPVNITSNVHTVSLPPASETFPSGTLCWVTGWGNINNDVSLPPPFPLEEVQVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 GVVSWGEGCAQPNRPGIYTRVTYYLDWIYRYVPK 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AEOWYLTAAHCF-RNTSETSLYQYLLGARQLYQPGPHAMYARYRQYESNPLYQGTASSAD 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGS---HFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 02210-2211
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                                   LENGTH: 274 amino TYPE: amino acid STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/016,366A
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                       TOPOLOGY: linear
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                                                                                                                                                             617-720-2441
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N: 530
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GENERAL INFORMATION:
                                                                                                                                                                                      FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08978404B
                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
              TOPOLOGY: 11
                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FBSTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILLING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                   LENGTH: 274 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 GVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
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                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 GVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPK 272
                                                                                                                                                                         TELEFAX: 617-720-244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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VENTION: MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                   Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
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43.8%; Pred. No. 3.8e-57;
tive 46; Mismatches 99; Indels 9
                                                                                                                                                                                                                                                                                                                             60/032,354
                                                                                                                                                                                                                               B0801/7090
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9

Query Match

37.5%; Score 588.5;

DB 2;

Length 274;

Best Local Similarity Matches 120; Conserv

Conservative

DB 2; 99;

Length 273;

9;

Gaps

4;

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US-09-016-366A-19
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US-09-016-366A-19
                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19,
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 43.8 Matches 120; Conservative
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                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: 617-720-3500
                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
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APPLICANT: Huang, Chifu
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                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 600 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: U.S.A.
02210-2211
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                                                                                                                            linear
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                                                                                                                                             single
37.4%; Score 587.5; DB 2
43.8%; Pred. No. 4.9e-57;
ative 46; Mismatches 99
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245

US-08-978-404B-14

ENERAL INFORMATION:
APPLICANT: Stevens,
TITLE OF INVENTION:
TITLE OF INVENTION:

Stevens,

NUMBER OF SEQUENCES:

CITY: Boston STREET:

600 Atlantic Avenue

COUNTRY:

U.S.A.

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

02210-2211 X X

COMPUTER:

IBM Compatible

RIOR APPLICATION DATA:

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LLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNG---SHFCGGSLI 65
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ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTA 64

4.

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Matches

120;

Conservative

Query Match
Best Local Similarity

37.48;

US-08-978-404B-14

STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: No. 5968782e

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids TYPE: amino acid

TELEPHONE: 617-720-35
TELEFAX: 617-720-2441

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Sequence 14, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/032,354
FILING DATE: 04 DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard L.
MAST CELL PROTEASE THAT CLEAVES
  46;
                   Score 587.5; DB 2; Pred. No. 4.9e-57;
    Mismatches
                                       Length 273;
    Indels
  9;
  Gaps
    4;
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                                                                                                                                                   US-09-016-366A-23
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Patent No. 5955431
                                                              Query Match
Best Local :
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/037,090 FILING DATE: 05-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 GVISWGEGCARONRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 HPQWVLTAAHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGAD 119
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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17 SQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQ---RNGSHFCGGSLIAEQWVLTA 73
                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEQWVLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQA
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                                                                 Similarity
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                                                                                                                                                                                                                             267 amino acids
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                                             Conservative
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                                                                                                                                                                       linear
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                                                                                                                                                                                        single
                                             36.8%; Score 578.5; DB 2;
43.6%; Pred. No. 4.7e-56;
tive 45; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                              36,637
                                                                                                                                                                                                                                                                                                                                                                                 B0801/7093
                                               Indels
                                                                                    Length 267;
                                               9
                                               Gaps
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US-08-978-404B-18
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                                                                                                            Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acid
TYPE: amino acid
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APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: 517-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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ent No. 5968782
NERAL INFORMATION:
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240 CAQPNRPGIYTRVTYYLDWIHHYVPK 265
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         74
                                                          STRANDEDNESS:
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                                                                                                                              Local Similarity
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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COMPUTER: IB
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ZIP: 02210-2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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AHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEA 132
                                  ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGADIALLELEE 121
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                                                                                                              Conservative
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                                                                                                      36.8%; Score 578.5; DB 2;
43.6%; Pred. No. 4.7e-56;
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240 CAOPNRPGIYTRVTYYLDWIHHYVPK 265
            253 CARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                            133 PVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCN 192
                                                                                                                                                                   65 AHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGADIALLELEE 121
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Search completed: August 13, 2002, 08:56:22 Job time: 209 sec



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Maximum DB seq length:
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21: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\Aa199.DAT:*
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                  HTRM clone 3376404
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Amino acid sequence Amino acid sequence	mast e mMCP	cell	00	mast cell t	mast cell t	Human mast cell tr	il homo	acid sequen	(U	cid sequen	n gen	Amino acid sequenc	e		S	Amino acid sequenc	Human novel secret	m	Human serine prote	Human novel secret	Human novel secret	Novel human enzyme	Human serine prote		Human serine prote	ጥ	Human serine prote

# ALIGNMENTS

AAY73388;

AAY73388 standard; Protein;

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24-FEB-2000

(first entry)

Hillman Gerstin 05-MAY-1998; 07-AUG-1998; 02-OCT-1998; HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment. WPI; 2000-052941/04. N-PSDB; AAZ52473. 04-MAY-1999; HTRM clone 3376404 protein sequence. (INCY-) INCYTE PHARM INC. 11-NOV-1999. WO9957144-A2 Homo sapiens EH, Bandman O, Patterson C, 98US-0084254. 98US-0095827. 98US-0102745. 99WO-US09935 Lal P, Baughn Yue H, Reddy R, n MR, Azimzai Y, Tang YT; Lu DAM;

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CC AAY73325-Y73389 are human transcriptional regulator molecule (HTRM) CC for preventing or treating disorders associated with decreased expression CC or activity of HTRM which include cell proliferative disorders such as CC arteriosclerosis and cirrhosis; cancers including adenocarchoma and Cleukaemia; immune disorders such as AIDS, Addison's disease, diabetes CC mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus CC erythematosus, and myasthenia gravis; infections and trauma. Antagonists CC of the HTRM polypeptides are useful for treating or preventing disorders CC associated with increased expression or activity of HTRMs. HTRM CC polypeptides, their immunogenic fragments or oligopeptides are useful CC for screening libraries of compounds in drug screening techniques. CC Polynucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRMs. Pectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression. Antibodies which specifically bind HTRM and polynucleotides encoding HTRM are useful for diagnosing disorders associated with the expression of HTRM. Nucleotide Sequences encoding HTRM may be useful to generate hybridization probes CC differences in gene sequences among normal, carrier and affected CC differences in gene sequences among normal, carrier and affected CC the appearance of clinical symptoms and thereby progression of cancer can be prevented by aggressive treatment or preventive measures.
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Best Local :
Human secretory and transmembrane; PRO; mammalian; cancer; breast; prostate; cervical; tumour necrosis factor-alpha; T cartilage; ear; proliferation; glucose; free fatty acid; sk
                                                                                                                                   Human PRO4327
                                                                                                                                                                                                                                                                                                              AAU12282 standard;
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PRO polypeptides, and to detect the presence of mammalian lung, colon, cc breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha ("NP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or correct cells, the release of proteoglycans from cc cartilage, the proliferation of inner ear utricular supporting cells or cartilage, the proliferation of finner ear utricular supporting cells or cof T-lymphocytes, the release of a cytokine from peripheral blood composites (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding
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PRO
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PRO
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                                                                                                                                                                                                                                                                                                                   Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
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01-MAR-2000;
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be used to generate probes,
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                                                                                                                                                                                                                                                                                                                                        foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; negioner; kidney disorder; gastrointestinal disorder; allergy; regnancy-related disorder; endocrine disorder; infection; wound healing; there; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene 4 encoded secreted protein HWHIH10, SEQ ID NO: 67.
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                                                                                   19-NOV-1999;
21-JUL-2000;
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                            Ruben SM,
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                                                       (HUMA-) HUMAN GENOME SCI INC.
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                             Komatsoulis GA, Birse CE,
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                                                                                  99US-0166414.
2000US-0219665.
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/label- Signal_peptide
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Pred. No. 1.3e-134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted protein genes, and AAB03810-AAB03870 represent the proteins they encode. AAB03871-AAB03870 represent the proteins they encode. The secreted proteins and their genes are useful for preventing, the treating or ameliorating medical conditions, e.g., by protein or gene therapy, Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 482-483; 553pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosorbent assay (ELISA). The psecreted protein of the invention.
AAB73945;
                                            AAB73945 standard;
                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                      241 wlqagviswgegcarqnrpgvyirvtahhnwihriipklqfqparlggqk
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                                                                                                                                                                                                                                        SSADVALVELEAPVPETNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                       WLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQX 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSLIAEQWYLTAAHCFRNTSETSLYQYLLGARQLYQPGPHAMYARVRQVESNPLYQGTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1571; DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3e-134;
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29-MAY-2001

(first entry)

Human protease

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RESULT
AAM39388
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Best Local
 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human protease T protein. The protein is useful for treating a condition mediated by protease T. It is useful for treating an imbalance of desquamation, by topical application of a pharmaceutical composition containing the protease. The composition is useful as a topical skin care composition. It is useful as a laundry detergent, shampoo, hard surface cleaning composition, and dish care cleaning composition. Protease T protein is useful for treating and preventing skin flaking. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a non-natural
                                                               AAM39388 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 1; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New serine protease termed preventing skin flaking or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protease T; serine protease; dermatological; desquamation;
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                                                                                                ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFC 60
                                                                                                                                                          WLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQK 290
                                                                                                                                                                                                                                                                      ssadvalveleapvpftnyilpvclpdpsvifetgmncwvtgwgspseedllpeprilqk 180
                                                                                                                                                                                                                                                                                                                                                       GGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTA 120
                                                                                                                                         wlqagviswgegcarqnrpgvyirvtahhnwihriipklqfqparlggqk 290
                                                                                                                                                                                                                           LAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLYGQS
                                                                                                                                                                                                        lavpiidtpkcnllyskdtefgyqpktikndmlcagfeegkkdackgdsggplvclvgqs
                                                                                                                                                                                                                                                                                                     SSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQK 180
                                                                                                                                                                                                                                                                                                                                    ggsliaeqwvltaahcfrntsetslyqvllgarqlvqpgphamyarvrqvesnplyqgta
                                                                                                                                                                                                                                                                                                                                                                                                   \verb|mrrpaavplilllcfgsqrakaatacgrprmlnrmvggqdtqegewpwqvsiqrngshfc|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             care; laundry; detergent; shampoo; skin flaking.
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(first entry)
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                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1571; DB 22; 100.0%; Pred. No. 1.3e-134;
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imbalance of desquamation -
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맑 δÃ В

61

61 ggsliaeqwvltaahcfrntsetslyqvllgarqlvqpgphamyarvrqvesnplyqgta

120

GGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTA 120

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFC

Matches Query Match Best Local (

Similarity

99.68;

Score 1565; DB 22; Pred. No. 4.4e-134;

Conservative

0;

Mismatches

Indels Length

Gaps

0;

60 60

290; 0,

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immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                          assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                   utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 Sequence
                               specification
                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 2533; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemothetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  teukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Z,
Zhou P,
290 AA;
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2000US-0693036.
2000US-0727344.
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2000US-0620312
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2000US-0552317
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Wehrman T,
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Xu C, Xue
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Xue AJ,
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Yang Y,
                                                                                                                                                                                                                                                                                                                                         treating disorders
                                         part of the printed
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Zhang
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RESULT
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune System suppression, Activin/Inhibin activity, Chemotactic/Chemokinetic activity, Deemostatic
                                                                                                                                                                                                                                                                                                        Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM41174 standard;
                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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19-OCT-2000;
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                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                  HYSE-) HYSEQ INC
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   thrombolytic
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                                                                                                                                                                                                                                                                                                       , Liu C,
Wang z,
, zhou P,
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                                                                                                                                                                                     SEQ ID NO 6105; 10078pp; English.
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2000US-0553317.
2000US-0598042.
2000US-0520312.
2000US-0620312.
2000US-063450.
2000US-063191.
2000US-0693036.
2000US-0727344.
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Wehrman T,
Goodrich F
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cancer diagnosis
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e AJ,
RT;
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Yang Y,
                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                treating disorders
                                                                                                                                                                                                                                                                                                                       Zhang
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RESULTA
AAW77304
ID AAW7
XX AW7
AC AAW7
AC AAW7
XX O7-2
XX O7-2
XX Seri
XX BCON
KW Semi
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Best Local
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Note: The sequence data for this patent did not form part of the printed
             Disulfide-bond
                                                          Disulfide-bond
                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                          Serine protease; regulation; cell activity; viability; HELA2; ATC2; BCOM3; testisin; fertility; suppressor; testicular germ cell cancer seminoma; testis-specific expression; antitumour; sperm development infertility; human; chromosome 16pl3.3.
                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                     Misc-difference
                                                                                                        Disulfide-bond
                                                                                                                               Disulfide-bond
                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                  Disulfide-bond
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                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of SP003LA, a homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLYGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggsliaeqwvltaahcfrntsetslyqvllgarqlvqpgphamyarvrqvesnplyqgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                   /note=
205
                                                                                                         /note-
167
                                                                                                                                                       /note=
                                                                                  190
                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                            Location/Qualifiers
  /note=
                                                                                                                                          /note=
                                                                     note-
                          'note=
                                                                                              'note-
                                                                                                                                                                                        'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%;
97.9%;
                                                                                                                                                                                        "likely to be a catalytic
                                                                                                                                                                                                             "likely to be involved in
"likely
                       "likely to
                                                                                                                                          "likely to be a catalytic residue"
                                                                                                                                                                 "likely to
                                                                                                                                                                                                                                      "likely to be involved in
                                                                                            "likely to
                                                                                                                   "likely
                                                                                                                                                                                                                                                                                                                                                                                                                                            297
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Pred. No. 1.
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                                                                      be
                                                                                            be involved in disulphide bonding'
                                                                                                                                                                 be involved in
                       be a catalytic residue"
                                               be involved in
                                                                                                                    be involved in
  involved
                                                                      involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2e-130;
                                                                                                                                                                                                                                                                                                                                                                     HELA2
                                               disulphide bonding"
                                                                      disulphide
                                                                                                                   disulphide
                                                                                                                                                                 disulphide
                                                                                                                                                                                        residue"
                                                                                                                                                                                                                disulphide
                                                                                                                                                                                                                                      disulphide bonding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                        development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328;
                                                                     bonding"
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                                                                                                                   bonding
                                                                                                                                                                  bonding"
                                                                                                                                                                                                                bonding'
                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9836054-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW77302-04 represent HELA2 homologues. The genes are found in a cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; Fig 20C; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antalis TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMRA-) AMRAD OPERATIONS PTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1997;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1998
                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELA2 used for modulation
                                                                                                                                                         121
                                                                                                                                                                                           146
                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                 26 CGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSL 85
                                                                                                                                                                                                                                                                                                            1 cgrprmlnrmvggqdtqegewpwqvsiqrngshfcggsliaeqwvltaahcfrntsetsl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine protease(s) and kinase involved in regulating cell ivity and viability - particularly the testis-specific protease A2 used for modulation of fertility and as tumour suppressor
                                    TAHHNWIHRIIPKLQFQPARLGGQK 290
                                                                                                                                                                         PDPSVIFETGMNCWTTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQP
                                                                                                                                                                                                                                                    YQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILFVCL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-480768/41.
                                                                        ktikndmlcagfeegkkdackgdsggplvclvgqswlqagviswgegcarqnrpgvyirv
                                                                                                               \tt KTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRV
                                                                                                                                                   pdpsvifetgmncwvtgwgspseedllpeprilqklavpiidtpkcnllyskdtefgyqp
                                                                                                                                                                                                                                  yqvllgarqlvqpgphamyarvrqvesnplyqgtassadvalveleapvpftnyilpvcl
                                                                                                                                                                                                                                                                                                                                                                                           265;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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97AU-0005101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "likely to
                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 1449; DB 19; 100.0%; Pred. No. 1.6e-123; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTD.
265
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             297;
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RESULT AAB73946 ID AAB7

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AAB73946 standard; Protein;

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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a protease T fusion protein. Protease T is useful for treating a condition mediated by protease T. It is useful for treating an imbalance of desquamation, by topical application of a pharmaceutical composition containing the protease. The composition is useful as a topical skin care composition. It is useful as a laundry detergent, shampoo, hard surface cleaning composition, and dish care cleaning composition. Protease T protein is useful for treating and preventing skin flaking. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a non-natural
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 4; 83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; protease T; serine protease; dermatological; desquamation; skin care; laundry; detergent; shampoo; skin flaking; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New serine protease termed preventing skin flaking or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF77000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-265889/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2000; 2000WO-US23823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200116293-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zymogen activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
   290
                              273
                                                                                           213
                                                                                                                        170
                                                                                                                                                      153
                                                                                                                                                                                    110
                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                            33
               HRIIPKLQFQPARLGGQK 290
                                                                           LCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWI
                                                                                                                                        ETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDM
                                                                                                                                                                                                 RQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIF 152
                                                                                                                                                                                                                                             dkivggyaleegewpwqvsiqrngshfcggsliaeqwvltaahcfrntsetslygvllga 109
                                                                                                                        etgmncwvtgwgspseedllpeprilqklavpiidtpkcnllyskdtefgyqpktikndm
                                                                                                                                                                                 \verb|rqlvqpgpham|| yarvrqvesnplyqgtassadvalveleapvpftnyilpvclpdpsvif|
                                                                                                                                                                                                                                                                            NRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGA
hriipklqfqparlggqk 307
                                                            lcagfeegkkdackgdsggplvclvgqswlqagviswgegcarqnrpgvyirvtahhnwi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein of protease T in a zymogen activation construct.
                                                                                                                                                                                                                                                                                                                                                                                     315 AA;
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andrade-Gordon
                                                                                                                                                                                                                                                                                                                         87.4%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease T, useful for treating
imbalance of desquamation -
                                                                                                                                                                                                                                                                                                         Score 1373; DB 22;
Pred. No. 1.4e-116;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                      This polypeptide, termed HE2NW40, comprises a serine protease that that shows homology to human tryptase. Its amino acis sequence was deduced from an isolated cDNA clone (see AAX06942). HE2NW40 polypeptides and polypucleotides are useful for diagnosing diseases related to over or underexpression of HE2NW40 protein by identifying mutations in the HE2NW40 gene, and/or analysing the presence or amount of expressed polypeptide (claimed). HE2NW40 polypeptides, olypucleotides (gene therapy), antisense sequences, agonists and intagonists, and soluble polypeptides that bind the HE2NW40 ligand to prevent expression, can be used to modulate HE2NW40 expression or activity. Diseases diagnosed, prevented or treated include cancer, inflammation, asthma, wasting diseases, atherosclerosis, or activity, diseases diagnosed, prevented or treated include cancer, inflammation, asthma, wasting diseases, atherosclerosis, of disorders including Alzheimer's disease. HE2NW40 antibodies are cuseful for inducing an immune response to immunise and prevent cuseful for inducing an immune response to immunise and prevent consequences, and for isolating HE2NW40 clones or purifying the polypeptide by affinity chromatography. HE2NW40 polypeptides can disease administered directly or as a vaccine to inoculate against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW88453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1998;
10-JUN-1997;
17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New serine protease HE2NW40 polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of cancer, Alzheimer's disease and asthma
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-072882/07.
N-PSDB; AAX06942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HE2NM40; serine protease; human; cancer; inflammation; asthma; wasting disease; atherosclerosis; stroke; diabetes; arthritis; neurodegenerative disease; Alzheimer's disease; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease HE2NW40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1999
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61 GGSLIAEQWYLTAAHCFRNTSETSLYQYLLGARQLYQPGPHAMYARVRQYESNPLYQGTA 120
                                                                                                                                            Local Similarity
les 234; Conserv
                                                      9

    Page 16-17; 21pp; English.

                                                                                                                                                                                                                                    304 AA;
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clinkenbeard HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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97GB-0012088.
97EP-0308295.
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                                                                                                                                                        76.2%;
82.1%;
                                                                                                                                     Score 1197; DB 20;
Pred. No. 1.3e-100;
7; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southan CD;
                                                                                                                                     Indels
                                                                                                                                                                        Length 304;
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RESULT :
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05-JAN-1998;
05-APR-1998;
29-APR-1998;
10-JUN-1998;
This sequence represents human PRO343 (UNQ302), a protein encoded by the novel cDNA clone DNA43318 (see AAX87259). Amplification of DNA43318 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO343 may have use in cancer tharapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis
                                                                                                                                                                                                             WPI; 1999-430385/36.
N-PSDB; AAX87259.
                                                                                                                                                                                                                                              Botstein D, Godd.
Roy MA, Wood WI;
                                                                                                                                            Example 1; Fig 12; 162pp; English.
                                                                                                                                                                       Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                 10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9935170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO343; UNQ302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour-associated protein PRO343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06482 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 WLQAGV-ISWGEG-----CARQNRPGVYIRVTAHHNWIHRIIPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ggsliaeqwvltaahcfrntsetsldqvllgarqlvqpgphamyarvrqvesnplyqgta 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fqptgpgqgwglgpvpwvmlqteppsvlirvngqqnwihrimpkl 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQK 180
                                                                                                                                                                                                                                                             Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                         98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
98US-0088742.
                                                                                                                                                                                                                                                                                                            9805-0107783
                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US00106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; tumour; diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "mature protein"
                                                                                                                                                                                                                                                            Gurney AL,
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                                                                                                                                                                                                                                                     and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnostic kits.
                                                                                                                                                                                                                                     Sequence
                                    317 AA;
                                                                                                                                                                                          4;
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Search completed: August 13, 2002, 08:56:59 Job time: 136 sec

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Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Maximum DB seq length: 200000000
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SPTREMBL_19:*

1: sp_archea:*

2: sp_bacteria

3: sp_fungl:*

4: sp_human:*

5: sp_inverteb

6: sp_mammal:*

7: sp_mhc:*

8: sp_organel:

9: sp_bage:*

10: sp_phage:*

11: sp_rodent:

12: sp_vrius:*

13: sp_vrius:*

14: sp_unclass

15: sp_bacteri

17: sp_archea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
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1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fung1:*
                                                                                                                                                           sp_mammal:*
sp_mhc:*
sp_vodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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                                                                                                              sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

45	44	43	42	41	40	39	38	37	36	35 5	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
445.5	446.5	446.5	448	448	449.5	450.5	452.5	453	454.5	455	462	462.5	467.5	469	471	477	478.5	481.5	483	484	485.5	486	486.5	494.5	498.5	500.5	503	503
28.4	28.4	28.4	28.5	28.5	28.6	28.7	28.8	28.8	28.9	29.0	29.4	29.4	29.8	29.9	30.0	30.4		30.6										
767	263	260	415	279	845	263	263	326	279	467	329	855	405	1524	492	624	537	812	624	267	624	282	581	490	322	812	810	454
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Q9DGR2	Q9D8X8	Q9W7Q3	Q29015	Q9QZ74	Q9DGR1	Q9DC86	Q9CR35	Q9D9M0	Q99MS4	Q967X8	Q9GL10	Q9JJI7	Q96E86	Q91674	Q96T73	Q91Y47	Q9BYE1	Q91WJ5	Q9DAT3	Q9BK47	Q95ME7	Q9D4I3	Q9BYE2	Q920K3	Q920S2	Q9R0W3	Q15146	046506
Q9dgr2 xenopus lae	mus musc	Q9w7q3 paralichthy	Q29015 sus sp. pre	Q9qz74 rattus norv	Q9dgrl xenopus Lae		Q9cr35 mus musculu	mus	mus	panul	Q9g110 ovis aries	Q9jji/ rattus norv	- 3	4 xen	Q96t73 homo sapien	/ mus	OWOL	. mus	mus	-	Q95me7 oryctolagus	Q9d413 mus musculu	Domo				-	

# ALIGNMENTS

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EMBL; ANDOS642; CAAO6644.1;  HSSP; P00763; 1DPO.  MEROPS; S01.252;  InterPro; IPR001314; Chymotrypsin.  InterPro; IPR001314; Chymotrypsin.  InterPro; IPR001254; Trypsin.  Pfam; PR00089; trypsin; 1.  Pfam; PR00722; CHYMOTRYPSIN.  PRINTS; PR00722; CHYMOTRYPSIN.  PRART; SM00020; TRYPSIN_HOM; 1.  PROSITE; PS00134; TRYPSIN_DOM; 1.  PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.  PROSITE; PS00135; TRYPSIN_LSE; 1.  Hydrolase; Protease; Serine protease; Signal.  Hydrolase; Protease; Serine Protease; Signal.  NON_TER  1	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  STRAIN=FISHER; TISSUE=BRAIN;  STRAINE=98389725; PubMed=9722524;  MEDLINE=98389725; PubMed=9722524;  Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe R.;  "Serine Proteases in Rodent Hippocampus.";  J. Biol. Chem. 273:23004-23011(1998).  -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.	01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SERINE PROTEASE PRECURSOR (FRAGMENT). BSP2. Rattus rattus (Black rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10117;	LT 1 81 80 088781 PRELIMINARY; PRT; 297 AA.

DB 11;

Length

297;

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Best Local :
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                                                                                                                                                                                                       Pfam; PF00009; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PVX7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                       "The expression control of xepsin by non-axial and planar posteriorizing signals in Xenopus epidermis."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AB018694; BAA84941.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PVX7
                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.UPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBI_TaxID=8355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 QGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPR 176
85 LYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVC 144
                                                                       25 ACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETS
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AGSILTNRWYVSAAHCFSSNMDKPSPYSVLLGAWKLGNPGPRSQKVGIASVLPHPRYSRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGSLIAEQWVLTAAHCF-RNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLY--- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PAAVPLLLLL----CFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFC
                                          ACGVPVISNRIVGGMDSKRGEWPWQISLSYKSDSICGGSLLTDSWVMTAAHCI-DSLDVS 74
                                                                                                                                                                                                                                                                                                                                                                                TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGT--HADIALVRLERPIQFSERILPICLPDSSVHLPPNTNCWIAGWGSIQDGVPLPRPQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLQKLKYPIIDPELCKSLYWR----GAGQEAITEDMLCAGYLEGKRDACLGDSGGPLMCQ 239
                                                                                                                                                                              Protease; Serine protease.
389 AA; 42375 MW; B31FB4A2F5D1F6E3 CRC64;
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                                                                                                           Conservative
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                                                                                                                      43.4%;
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                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 b; Score 721.5; DB
b; Pred. No. 2e-63;
42; Mismatches
                                                                                                                    Score 682.5; DB 1
Pred. No. 2.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
                                                                                                          Mismatches
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                                                                                                                                    DB 13; Length 389;
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

Hydrolase; Protease; Serine protease.

SEQUENCE 317 AA; 34413 MW; EEC78A9F46D138FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
     262
                                    208
                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB038496; BAB08216.1; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Xenopus laevis."
Gene 252:209-216(2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada K., Takabatake T., Takeshima K.; Isolation and characterization of thre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
EMBRYONIC SERINE PROTEASE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DGR3;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 PDFSFIQEDMYCAGYKEGRIDACQGDSGGPLYCNYNNVWLQLGIVSWGYGCAEPNRPGVY
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                                                                                                                                                                                                                                                                  22 AATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 YYTVYLGAYQLSAPDNSTVSRGVKSITKHPDFQYEGSSGDIALIELEKPVTFTPYILPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY
                                                                                               PICLPASPVTFSSGTECWITGWGQTGSEVPLQYPATLQKVMVPIINRDSCEKMYHINSVI 207
YIRVTAHHNWI-HRIIPKLQFQP 283
                                 SETEILIQSDQICAGYQAGQKDGCQGDSGGPLVCKIQGFWYQAGIVSWGERCAAKNRPGV
                                                           GYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLYCLYGQSWLQAGYISWGEGCARQNRPGY 261
                                                                                                                                 PVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEF 201
                                                                                                                                                                LPSGCGVRLGAYQLYVKNPHEMTVKVDIIYINSEFNGPGTSGDIALLKLSSPIKFTEYIL 147
                                                                                                                                                                                               ETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYIL 141
                                                                                                                                                                                                                                  APPLCGSPVFSSRIVGGTDTRQGAWPWQVSLEFNGSHICGGSIISDQWILTATHCIEHPD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P--KTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQ 204
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus.
                                                                                                                                                                                                                                                                                                                    43.1%;
                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                               Score 677.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                three novel serine protease genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                 94; Indels
                                                                                                                                                                                                                                                                                                                                  Length 317;
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                                                                                                                                                                                                                                                                                                 Gaps
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268 YTFVPAYETWISERSV--ISFKP

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Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                       O90YZ9
O90YZ9;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DISTAL INTESTINAL SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
ISSUB-COLON;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010970; AAH10970.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO DISTAL INTESTINAL SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91XC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
Biochim. Biophys. Acta 1
-I- SIMILARITY: BELONGS
                            DISP.";
                                                                                   SEQUENCE FROM N.A. MEDLINE-20246299; PubMed-10786627;
                                                         Walters J.R.;
                                                                    Shaw-Smith C.J., Coffey A.J.,
                                                                                                                                              Mammalia; Eutheria;
                                                                                                                             NCBI_TaxID-10090;
                                          "Characterization of a novel murine intestinal serine
                                                                                                                                                                                                                                                                                                                                                239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RARCIFLLLLQILTRARGDILPSVCGHSRDAGKIVGGQDALEGQWPWQVSLWITEDG-HI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPAAVPLLLLLCFGSQRAK-AATACGRPRMLNRMVGGQDTQEGEWPWQVS--IQRNGSHF 59
                                                                                                                                                                                                                                                                                                                                                 SSWTQVGITSWGIGCARPYRPGVYTRVPTYVDWIQRIL 276
                                                                                                                                                                                                                                                                                                                                                                            QSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII 276
                                                                                                                                                                                                                                                                                                                                                                                                        QELAVPLLDSEDCEKMYHTQGSSLSGERIIQSDMLCAGYVEGQKDSCQGDSGGPLVCSIN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DASSGDIALVQLDTPLRPSQF-TPVCLPAAQTPLTPGTVCWVTGWGATQERDM---ASVL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRIL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33707 MW; FA126747DEAE0AB6 CRC64;
                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.3%;
 1490:131-136(2000)
S TO PEPTIDASE FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 633.5;
Pred. No. 1.1
                                                                       Leversha M.,
                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 1.1e-54;
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   FAMILY
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                                                                        Freeman T.C.,
   S1;
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 ALSO
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    KNOWN
                                           protease
                                                                        Bentley D.R.,
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SOUR DESCRIPTION OF THE PROPERTY OF THE PROPER
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Q96RZ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; Pr00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_HS; II

PROSITE; PS00134; TRYPSIN_HS; II

PROSITE; PS00135; TRYPSIN_SER; 1

Hydrolase; Protesse; Serine prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96RZ8;
Q96RZ8;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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EMBL; AJ243866; CAB56465.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1353645; Disp.
InterPro; IPR001314; Chymotrypsin
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                       "Sequence, structure and pathology of the fully annotated Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001). EMBL; AE006466; AAK61269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01
                                                                                                                                        Transmembrane. SEQUENCE 321 AA; 33829 MW;
                                                                                                                                                                                                                                                                                                                          MEDLINE-21096910; PubMed-11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                        Higgs D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 CGGSLIAEQWYLTAAHCFRNTSETSLYQYLLGARQLYOPGPHAMYARVRQYESNPLY-QG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RARCIFLLLLQILTRARGDILPSVCGHSRDAGKIVGGQDALEGQWPWQVSLWITEDG-HI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DASSGDIALVQLDTPLRPSQF-TPVCLPAAQTPLTPGTVCWVTGWGATQERDM----ASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSWTQVGITSWGIGCARPYRPGVYTRVPTYVDWIQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QELAVPLLDSEDCEKMYHTQGSSLSGERIIQSDMLCAGYVEGHIDSCQGDSGGPLVCSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGSLIHEVWVLTAAHCFRRSLNPSFYHVKVGGLTLSLLEPHSTLVAVRNIFVHPTYLWA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease; Serine protease.
310 AA; 33701 MW; F828EC7F6D25303F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
BRANE TRYPTASE, GENE NAME TMT, AF175522_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.7%;
                             39.0%; Score 612.5;
47.3%; Pred. No. 1.
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     36;
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Pred. No. 1.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN_1.
                                                                                                                                              FFF5089EDC4FC73D CRC64;
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        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321
                                     .5e-52;
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                                                          DB 4;
           91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 310;
                                                             Length 321;
           Indels
                                                                                                                                                                                                                                                                                       terminal 2
           17;
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           Gaps
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                                                                             Matches
                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00154; Trypsin.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp, SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                    Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC003851; AAH03851.1; -.
SMBL; AF378086; AAL06320.1; -.
MBL; AF378085; AAL06319.1; -.
ISSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/SVJ AND SWISS; TISSUE=LUNG;
STRAIN=129/SVJ, AND SWISS; TISSUE=LUNG;
Verghese G.M., Caughey G.H.;
"Molecular cloning and characterization of mouse prostasin, a type I
"membrane-associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO PROTEASE, SERINE, 8 (PROSTASIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
14 AVTILLLIGLLQSGIRADGTEASCGAVIQP----RITGGGSAKPGQWPWQVSITYDGNHV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AGVISWGEGCARQNRPGVYIRVTAHHNWIHRII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 PIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLYCLYGQSWLQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 DIALVELSVPVTLSSRILPVCLPEASDDFCPGIRCWVTGWGYTREGEPLPPPYSLREVKV
                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 SVVDTETCRRDYP-----GPGGSILQPDMLCA---RGPGDACQDDSGGPLVCQVNGAWVQ
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                              AVPLILLLCF----GSQRAKAATACG----RPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGIVSWGEGCGRPNRPGVYTRVPAYVNWIRRHI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWYTGWGSPSEEDLLPEPRILQKLAV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPOWVLTAAHCFSGSLNSSDYQVHLGELEITL-SPH--FSTVRQIILHSSPSGQ-PGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AECWVLTAAHCFRNTSETSLYQYLLGARQLVQPGPHAMYARVRQV--ESNPLYQGTASSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLLLCFGSQRAKAATACGRPRMLN---RMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLLAVPGVSLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRLRRVHVCGGSLL
                                                                                            Similarity
                                                                                                                                                                Protease; Serine protease, 339 AA; 36216 MW; BC2DE
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   luvs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                          38.9%; Score 610.5; DB 1 42.3%; Pred. No. 2.5e-52;
                                                                           48;
                                                                                                                                                                BC2DE88BC057AF10 CRC64;
                                                                       Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
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                                                                                                        DB 11; Length 339;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 123;
                        Q96RZ6;
Q96RZ6;
01-DEC-2001
01-DEC-2001
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TRYPTASE I.
               TRYPTASEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL
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                                                                                                                                                                           239
                                                                                                                                                                                       246 VISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                    121 ALLKLINPVNISDYVHEVPLPPASETFPSGTLCWVTGWGNIDNGVNLPPPFPLKEVQVPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 QLEVPLISRETCSCLYNINA-VPEEPHTIQQDMLCAGYVKGGKDACQGDSGGPLSCPMEG
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                                                                                                                                                                                                                                                                                                                                                               67 EQWVLTAAHCF-RNTSETSLYQVLLGARQLVQDGPHAMYARVRQVESNPLYQGTASSADV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 IWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                ø
sapiens
                                                                                                                                                                      VVSWGEGCAQPNRPGIYTRVTYYLDWIHRYVPK 271
                                                                                                                                                                                                                               IENHLCDLKYHKGLITGDNVHIVRDDMLCAG-NEG-HDSCQGDSGGPLVCKVEDTWLQAG
                                                                                                                                                                                                                                                       IDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAG 245
                                                                                                                                                                                                                                                                                                                                               PQWVLTAAHCVGPDVADPNKVRVQLRKQYLYY---HDHLMTVSQIITHPDFYIVQDGADI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLQTPRPLQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGSLIAEQWVLTAAHCERNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGT
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                                      l (TrEMBLrel. 19,
l (TrEMBLrel. 19,
l (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AA; 30332 MW;
                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
(Human)
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45.1%;
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                                      Last sequence update)
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                                                                   Created)
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Pred. No. 8.9e-50;
2; Mismatches 99
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RP SEQUENCE FROM N.A.

RC STRAIN-C578L/6J; TISSUE-LIVER;

RX MEDLINE-21085660; PubMed-11217851;

RX MEDLINE-21085660; PubMed-11217851;

RA ARAKWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konnoo H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
)1-DEC-2001 (TrEMBLrel.
1300008A22RIK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21096910; PubMed-11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DBIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oledeo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 VALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 HPQWVLTAAHCVGPDVKDLAALRVQLREQHLYY---QDQLLPVSRIIVHPQFYTAQIGAD 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equence, structure and pathology of the fully annotated terminal 2 of the short arm of human chromosome 16."; m. Mol. Genet. 10:339-532(2001).

BL. AE006466; AAK61271.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLALPVLASRAYAAPAPGQAVQRVGIVGGQEAPRSKWPWQVSLRVHDPYWMHFCGGSLI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQA
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Matches 111
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R PRINTS; PRO0261; LDLAECEPTOR.

R SMART; SM00042; CUB; 1.

R SMART; SM000192; LDLa; 3.

R SMART; SM00020; Tryp_SPc; 1.

R PROSITE; PS50180; CUB; 1.

R PROSITE; PS50180; TRYPSIN_DOM; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.

R PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

R PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

R PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Hayashizaki Y.;
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IPR000859; CUB.
IPR002172; LDL_recept_A.
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Search completed: August 13, 2002, 09:00:31 Job time: 248 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 13, 2002, 08:57:03; Search time 13.47 Seconds (without alignments) 833.606 Million cell updates/sec

Title: Perfect score:

US-10-041-006-7 1571 1 MRRPAAVPLLLLCFGSQRA.....WIHRIIPKLQFQPARLGGQK 290

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

al number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

DR MEROPS; S01.074; DR MEROPS; S01.074; DR InterPro; IPR0013 DR InterPro; IPR0012; DR Pfam; PF00089; tr DR PRINTS; PR00722; T DR SMART; SM00020; T DR PROSITE; PS50240;				AC Q9BQR3; DT 16-OCT- DT 16-OCT- DT 16-OCT- Marapsi	RESULT MPN_HUMAN ID MPN_
	This SWISS-PROT entry is copbetween the Swiss Institute the European Bioinformatics use by non-profit institute modified and this statement entitles requires a license or send an email to license	SEQUENCE FROM N.A. SEQUENCE FROM N.A. POITUNATO M., Dando P.M "Cloning, sequencing and proteinase."; Submitted (MAR-2001) to -1-SIMILARITY: BELONGS TRYPSIN FAMILY.	MPN. HOmo sapiens (Human). Eukaryota; Metazoa; C Eukaryota; Eutheria; F Mammalia; Eutheria; F	Q9BQR3; 16-OCT-2001 16-OCT-2001 16-OCT-2001 Marapsin pred	T 1 UMAN HUMAN
EMBL; AJ306593; CAC35467.1; MEROPS; S01.074;	S-PROT entry is copyright. the Swiss Institute of Biol ean Bioinformatics Institut non-profit institutions as and this statement is not r requires a license agreemen n email to license@isb-sib.	CUNATO M., DANDO P.M., DANDO P	(Human). etazoa; C theria; P 606;	(Rel. 40, (Rel. 40, (Rel. 40, cursor (E)	STANDARD;
EMBL; AJ306593; CAC35467.1; MEROPS; SO1.074; InterPro; IPR001314; Chymotrypsin. InterPro; IPR001254; Trypsin. Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN. SMARR; SM00020; Tryp_SPc; 1.	is copyrastitute of matics III institutititement is icense as icen		Chordata; Primates;	Created) Last seg Last ann C 3.4.21.	
C35467.1; ; Chymotrypsin. 4; Trypsin. psin; 1. HYMOTRYPSIN. TRYPSIN_DMM; 1. TRYPSIN_HIS; 1.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A., Rawlings N.D., Barrett A.J.; FORTUNATO M., Dando P.M., Rawlings N.D., Barrett A.J.; FORTUNATO M., Dando P.M., Rawlings N.D., Barrett A.J.; FORTUNATO M., Barre	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	Q9BQR3; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Marapsin precursor (EC 3.4.21).	PRT; 290
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
EMBL; AB010779; BAB20263.1; -.
                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 47-317 FROM N.A.

Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E., Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S., Goodwin L., Bryant J., Tesmer J., Melncke L., Longmire J., White Ueng S., Tatum O., Campbell C., Fawcett J., Deaven L.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9GZN4; 043342;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PISSUE-Pancreas;
long G.W., Stevens R.L.;
Identification of a new member of the chromosome 16 family of serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                     TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1571; DB 1; 100.0%; Pred. No. 1.3e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA
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17,

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RESULT 3
BSS4_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
            TISSUE-Brain;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
"Cloning and characterization of a novel serine protease, mBSSP-4.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                         Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
                                                                                                                                                                                                                                                        BSS4_MOUSE
Q9ER10;
                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                   PRSS26 OR BSSP4.
                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                   184 PIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                       244 AGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGG 288
                                                                                                                                                                                                                                                                                                                                                                                         201 PIIDSEVCSHLYWRGAGQG----PITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                141 DIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 DVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 TSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AEOWYLTAAHCFR-NTSETSLYQYLLGARQLYQPGPHAMYARYRQYESNPLYQ-GTASSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLLLC----FGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                   AGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; Signal
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                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
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BY SIMILARITY.
N-LINKED (GLONAC.
L -> M (IN REF. 3).
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Pred. No. 6.3e-60;
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CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                  306
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(BY SIMILARITY).
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RESULT PSSB_HU ID SB_HU ID SB_
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Best Local S
Matches 136
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1

PROSITE; PS00134; TRYPSIN_SER; 1

PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lydrolase;
iGNAL
CHAIN
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                              PSSB_HUMAN STANDARD,
Q16651; Q9UCA3;
Q1.607-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation updat
O1-MAR-2002 (Rel. 41, Cast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial-entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
   TISSUE=Prostate;
MEDLINE=95286644; PubMed=7768952;
                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGSLLTNRWVVTAAHCFKSNMDKPSLFSVLLGAWKLGSPGPRSQKVGIAWVLPHPRYSWK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVPLLLLLCFGSQRAKAATA-----CGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDDHWLLTGIISWGEGCA-DDRPGVYTSLLAHRSWVQRIVQGVQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQFQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLQKLKVPIIDSELCKSLYWR----GAGQEAITEGMLCAGYLEGERDACLGDSGGPLMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGT--HADIALVRLEHSIQFSERILPICLPDSSVRLPPKTDCWIAGWGSIQDGVPLPHPQ 193
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                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.38;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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; Pred. No. 4.9e-56;
47; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
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                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
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"Molecular cloning, tissue-specific expression, localization of human prostasin mRNA."; J. Biol. Chem. 270:13483-13489(1995).
                                                                                                                                         CHAIN
PROPEP
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 269:18843-18848(1994).
-I- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY
-I- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu J.X., Chao L., Chao J.; "Prostasin is a novel human serine proteinase from seminal fluid. Purification, tissue distribution, and localization in prostate
                                                                                     DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu J.X., Chao L., Chao J.;
            ACT_SITE
ACT_SITE
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CARBOHYD
                                                             DISULFID
                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L41351; AAC41759.1; -. EMBL; U33446; AAB19071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94308140;
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                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                     MIM; 600823;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC001462; AAH01462.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin. InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                  MEROPS;
SEQUENCE
                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                                                                                  Hydrolase;
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AA;
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        BY SIMILARITY.
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BY SIMILARITY.
CHARGE RELAY SYSTEM.
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CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . . )
                                                                                                                                                                                                                                   Zymogen; Signal; Glycoprotein;
                                                                                                                              SERINE PROTEASE
                                                                                                                                                                     PROSTATIN LIGHT PROSTATIN HEAVY
                                                                                                                                                                                                           POTENTIAL
                                                                                                                                           POTENTIAL
                                                                                                                                                                                               ACTIVATION PEPTIDE.
                                                                                                                 INTERCHAIN (BY SIMILARITY).
 -LINKED (GLCNAC. . .) (F
98DD6447F5A8C1B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGHT AND HEAVY, HELD
                                                                                                                                                                     CHAIN.
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             (POTENTIAL).
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Best Local :
               Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPES87; OPER01;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and expression of rat prostasin.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY
                                                                                 EMBL; AB017638; BAB20281.1; -. EMBL; AF202076; AAG32641.1; -.
                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE Kidney;
TISSUE=Kidney;

TISSOE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1998) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GSLIAEQWYLTAAHCFRNTSETSLYQYLLGARQLYQPGPHAMYARVRQYESNPLYQGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AVAILLYLGLLRSGTGAEGAEAPCGVAPQA--RITGGSSAVAGQWPWQVSITYEGVHVCG
                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: MEMBRANÉ-BOUND, SECRETED AFTER CLEAVAGE ITS C-TERMINUS (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AVPLLL---LLCFGSQRAKAATACG-RPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCG 61
                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULFIDE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                      TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                               IPR001254; Trypsin.
     Serine
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protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%; Score 618.5; DB 1 42.9%; Pred. No. 6.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyoshi T., Tomita K.;
the EMBL/GenBank/DDBJ databases.
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; Murinae; Rat
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _HUMAN
  SEQUENCE FROM N.A.

MEDLINE=99452974; PubMed=10521469;
Wong G.W., Tang Y., Feyfant E., Sa
Friend D.S., Krilis S.A., Stevens
                                                                                                       Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M., Wolters P.J., Verghese G.M.; Wolters P.J., Verghese G.M.; "Characterization of human gamma-tryptases, novel members of the chromosome 16p mast cell tryptase and prostasin gene families."; Immunol. 164:6566-6575(2000).
                                                                                                                                                                                                                                                                                                                                                                                                       Q9NRR2; Q9NRQ8; Q9C015; Q9UBB2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase). TPSG1 OR TMT.
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ACT_SITE
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                                                                                                                                                                                                                SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND MEDLINE-20302813; PubMed-10843716;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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TRANSMEM
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                                                                                                                                                                                                                                                                                                            Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 WLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LAVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LLLLLCFGSQRAK-----AATACG---RPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGSLVSNQWVVSAAHCFPREHSKEEYEVKLGAHQLDSFSNDIVVHTVAQIISHSSYREEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEVPLISRETCSCLYNINA-VPEEPHTIQQDMLCAGYVKGGKDACQGDSGGPLSCPIDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQGDIALIRLSSPYTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLQTPRPLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                           Metazoa;
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36843 MW;
                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.1%;
nt E., Sali A.,
Stevens R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 614.5; DB Pred. No. 1.4e-48
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I -> V (IN REF. 1).
A -> V (IN REF. 1).
; 5ED1AF05D9213B98 CRC64;
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CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                     Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
BY SIMILARITY.
POTENTIAL.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                     Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                      Li L.,
                                                                                                                                                                                                                                      GAMMA-2)
                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                        Li
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                    Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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Best Local S
Matches 129
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ACT_SITE
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EMBL; AF195508; AAF76458.1; -.
EMBL; AF175759; AAF03697.1; -.
EMBL; AF175522; AAF03695.1; -.
EMBL; AF223563; AAG48852.2; -.
                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Organization and alternative splicing of CACNAIH."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.-i- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outst he European Bioinformatics Institute. There are no restrictions se by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for an accordance to the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                   SEQUENCE
                                                                                                               CONFLICT
                                                                                                                                        VARIANT
                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a new member of the tryptase family of mouse and human mast cell proteases which possesses a novel COOH-terminal hydrophobic extension.";
                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                 DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mittman S., Agnew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 220-321 FROM N.A.
                                                                                                                                                                                                                                                                                                                    ISULFID
                                                 Local Similarity
               φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Expressed in many tissues.
POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
differ by 5 residues.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY. TRYPTASE SUBFAMILY.
LLLLLCFGSQRAKAATACGRPRMLN---RMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLI 65
                                                                                              160
321
                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease; Signal; Glycoprotein; Zymogen;
                                      Conservative
                                                                                                                                        288
                                                                                                                                                              204
                                                                                                                                                                                       132
                                                                                                                                                                                                                  126
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384
284
78
125
222
222
218
159
192
218
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274:30784-30793(1999).
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321
3044
78
125
225
145
220
228
228
60
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33827
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                                                                                                                                                              204
                                                                                                                                                                                       132
                                                39.1%;
                                                                                                  MW;
                                      36;
                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
                                                 Score 613.5; DB 1;
Pred. No. 1.6e-48;
                                                                                                               Σ
                                                                                                                                                                                                                                     M -> V (IN GAMMA-II).
                                                                                                                                       /FTId-VAR_012100.
L -> F (IN GAMMA-
                                                                                                                                                                          /FTId-VAR_012098.
S -> T (IN GAMMA-II).
/FTId-VAR_012099.
                                                                                                                                                                                                              /FTId-VAR_012097.
I -> M (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                    INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                              TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
                                                                                                              /FTId=VAR_012101.
W -> S (IN REF. 1
                                                                                                                                                                 ÿ
                                                                                                 FFF7B06E3C4A962D CRC64;
                                                                                                                                                                                                                                                                 SIMILARITY
SIMILARITY
                                      Mismatches
                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                     F (IN GAMMA-II).
                                                                                                                                                             I (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                    91;
                                                                                                                                                                                                                                                    .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
(BY SIMILARITY).
                                                             Length
                                      Indels
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                                      17;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
TPSG1 OR TMT.
Mus musculus (Mouse).
             CHAIN
CHAIN
                                                                                                                                                                                                        EMBL; AF175760; AAF03698.1; -. EMBL; AF175523; AAF03696.1; -. HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                         Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C., Friend D.S., Krilis S.A., Stevens R.L.;
"Identification of a new member of the tryptase family of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                        SIGNAL
                                                                               PROSITE; PS50240;
PROSITE; PS00134;
PROSITE; PS00135;
                                                                                                                                                           MGD; MGI:1349391; Tpsgl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99452974; PubMed=10521469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
TRANSMEM
                                                    Transmembrane.
                                                                    Hydrolase;
                                                                                                                                       PRINTS;
                                                                                                                                                  Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              human mast cell proteases which possesses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVVDTETCRRDYP-----GPGGSILQPDMLCA---RGPGDACQDDSGGPLVCQVNGAWVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQWVLTAAHCFSGSLNSSDYQVHLGELEITL-SPH--FSTVRQIILHSSPSGQ-PGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEQWYLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQV--ESNPLYQGTASSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLAVPGVSLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRLRRMHVCGGSLL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIVSWGEGCGRPNRPGVYTRVPAYVNWIRRHI 269
                                                                                             ; PR00722; CHINGE, ; PR00722; CHINGE, Spc; 1.
SM00020; Tryp_Spc; 1.
SM00020; TrypSIN_DOM;
TRYPSIN_DOM;
TRYPSIN_DOM;
                                                                    Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
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                                                                               TRYPSIN_HIS;
TRYPSIN_SER;
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                                                                  protease;
16
28
311
297
                                     4; 1.
.S; 1.
.ER; FALSE_NEG.
.Thal; Glycoprotein; Z
                                                                 Signal;
           TRYPTASE GAMMA LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel
             CHAIN
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                                                                  Zymogen;
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RESULT
PSS8_M
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Best Local (
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; (
dammalia; Eutheria; H
CBI_TaxID=10090;
[1]
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SEQUENCE
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ACT_SITE
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                                                                                                                                                                   Vuagniaux G., Vallet V., Fowler-Jaeger N., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.; "Activation of the amiloride-sensitive sodium channel by the mou serine protease mCAP1 expressed in a principal kidney cell line. Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SODIUM CHANNELS.
                 the
                                              This
                                                                                                 -I- SIMILARITY: BELONGS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ESD1;
16-OCT-2001
                                between
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Vuagniaux G., Vallet V.,
                                                                                                                                                                                                                                                                                                                                                                       Prostasin precursor PRSS8 OR CAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGT----ASSADVALVELEAPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 AVSGCGHPQVSNSGSRIVGGHAAPAGTWPWQASLRLHKVHVCGGSLLSPEWVLTAAHCFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 AATACGRPRMLN---RMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFR
                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                             DISULFIDE BOND (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-BOUND.
ITS C-TERMINUS (BY SIMILARITY).
                                                                       CAUTION: REF.1 SEQUENCE DIFFERS FRAMESHIFT IN POSITION 339.
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                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; C
Metazoa; Rodentia; C
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     institutions
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INTERCHAIN (POTENTIAL).
BY SIMILARITY.
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CHARGE (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 3e-4
38; Mismatches
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No. 3e-48;
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Query Match
Best Local S
Matches 118
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P50342;
01-OCT-1996
01-OCT-1996
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CARBOHYD
SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence upd
16-OCT-2001 (Rel. 40, Last annotation u
Mast cell tryptase precursor (EC 3.4.21
Meriones unguiculatus (Mongolian jird).
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
SEQUENCE FROM N.A STRAIN=MGS/SEA; T: MEDLINE=95366971;
                                                                                                                                                                     Mamma⊥1a;
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SIGNAL
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                                                                                                            NCBI_TaxID=10047;
                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
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                                                                                                                                                                  ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001254; Trypsin.
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  TISSUE=Intestine,
1; PubMed=7639711,
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Rodentia;
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INTERCHAIN (BY SIMILARITY).
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DARGE RELAY SYSTEM (BY SIMII CHARGE RELAY SYSTEM (BY SIMII N-LINKED (GICNAC. . . ) (POTEN N-LINKED M-LINKED (GICNAC. . . ) (POTEN N-LINKED M-LINKED M-LINKED M-LINKED M-LINKED M-LINKED M-LINKED M-
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Pred. No. 7.7e-48;
""cmatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MCT7\_RAT STANDARD; PRT; 273 AA.
P27435; P27436;
01-AUG-1992 (Rel. 23, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mast cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase,

Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus

MCPT7 OR MCP7.

NCBI\_TaxID=10116;

STRAIN-SPRAGUE-DAWLEY; SEQUENCE FROM N.A.

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SMART; SM00020; TRYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM,
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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"Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones unguiculatus, and its preferential expression in the intestinal mucosa.";
                                                   242
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                          LQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGS---HFCGG
                                                                                              QVPVVENQLCDLKYHKGVYTGDNIHIVRDDMLCAG-NEG-HDSCQGDSGGPLVCKVNGTW
                                                                                                                           AVPIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSW 241
                                                                                                                                                                                                 GADIALLELKNPVNISSHVHPVSLPPASETFPSGTLCWVTGWGNIDNDVSLPPPFPLKEV
                                                                                                                                                                                                                                               SADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKL 181
LQAGVVSWGEGCALPNRPGIYTRVTYYLDWIHRYVPK 268
                                                                                                                                                                                                                                                                                                                                                  SLIAEQWVLTAAHCFRNT-SETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTAS 121
                                                                                                                                                                                                                                                                                                                                                                                                     ALPLESLM----HRSPLCQEWG-----IVGGQEAPGNKWPWQVSLRANETYWRHFCGG
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                                                                                                                                                                                                                                                                                                    SLIHPQWVLTAAHCVGPTIADPNKVRVQLRKQYLYY---HDHLLAVSRIITHPTFYATQN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \begin{array}{c} 228 \\ 270 \end{array}
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Horil Y., Nawa Y.;
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MAST CELL TRYPTASE.

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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARIT
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Pred. No. 8e-47;
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Y SIMILARITY).
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induced rat mammary tumour."; Biochem. J. 283:209-216(1992) -I- FUNCTION: TRYPTASE IS THE

leupeptin-sensitive serine endopeptidase "Separation, purification and N-terminal

sequence analysis of a novel present in chemically

-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-,

FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL CELLS, AND IS SECRETED UPON THE COUPLED RESPONSE OF THIS CELL TYPE.

ACTIVATION-DEGRANULATION PROTEASE PRESENT IN MAST

with more restricted specificity than trypsin.
SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES

FAMILY S1; ALSO KNOWN AS

THE

MAST CELL ACTIVATION.

Eto

Grubbs C.

TISSUE=Breast carcinoma; MEDLINE=92231826; PubMed

PubMed=1314562;

SEQUENCE OF 29-51

"Tryptase from rat skin: purification and properties."; Biochemistry 30:4997-5007(1991).

different serine proteases and a carboxypeptidase A from various mast cell populations."; MEDLINE=97149430; PubMed=8996238; Lutzelschwab C., Pejler G., Aveskogh M., Hellman L.; "Secretory granule proteases in rat mast cells. Cloning of 10

rat

Braganza V.J., Simmons W.H.; "Tryptase from rat skin: pur STRAIN=SPRAGUE-DAWLEY; TISSUE-Skin; MEDLINE=91242400; PubMed=2036367;

SEQUENCE OF 29-53

Exp. Med.

185:13-29(1997).

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KEER BREEF B
                                                 PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                     PRINTS; PR00722; CHYMOTRYI SMART; SM00020; Tryp_SPc;
                                                                                                                                                                                                                        MEROPS; S01.026; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                           PIR; A23698; A23698.
PIR; S21275; S21275.
                        Hydrolase;
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                                                                                                                                                                                                                                                                                                                  HSSP; P20231; 1AAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: MAST CELLS.
PTM: GLYCOSYLATED (PROBABLE).
SIMILARITY: BELONGS TO PERTIDASE FAI
TRYPSIN FAMILY. TRYPTASE SUBFAMILY.
                                                                                                                                                                                                   PF00089;
                     Serine protease; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                         AAB48263.1; -.
                                                                                                                                                                    trypsin; 1.
2; CHYMOTRYPSIN.
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RESULT 10

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Search completed: August 13, 2002, 09:00:50 Job time: 227 sec
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45.6%; Pred. No. 1.7e-46;
tive 43; Mismatches 95; Indels 11
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ACTIVATION PEPTIDE.

ACTIVATION PEPTIDE.

MAST CELL PROTEASE 7.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

EX SIMILARITY.

BY SI
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Query: US-10-041-006-7
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Database sequences: 1797656
Database length: 1873333701
Search time (sec): 1855.110000
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-DB-(genEmb1 -QFMT-fastap -SUFFIX-p2n.rge -GapOp=12.000
-GAPOP=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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-EGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS-human40.dd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
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                                                                                  20 ATGAGGCGGCCGGCGGCGGTGCCGCTCCTGCTGCTGCTGTTTTGGGTC
                                                                                                                          1 MetArgArgProAlaAlaValProLeuLeuLeuLeuCysPheGlySe
                    rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
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Fortunato, M., Dando, P.M., Rawlings, N.D. and Barrett, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-MAR-2001) Fortunato M., MRC Molecular Enzymology Laboratory, Babraham Institute, Babraham Hall, Babraham, Cambr. CB2 4AT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1013) Fortunato, M.
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EGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII
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US-10-041-006-7
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TITLE
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Percent Similarity:
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      201 PheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGly...
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                                                 roIleIleAspThrProLysCysAsnLeuLeuTyrSerLysAspThrGlu
                                                                                                                                                                    IlePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSe
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                                                                                                            rGluGluAspLeuLeuProGluProArgIleLeuGlnLysLeuAlaValP
                                                                                                                                                       ATTTTTGAGACGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                         CCCTGGACCAGGTCCTGCGGGGCAAGGCAGTTAGTGCAGCCGGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGTGGGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGT
                                   CCATCATCGACACCCCAAGTGCAACCTGCTCTACAGCAAAGACACCGAG
                                                                                            TGAGGAAGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGC
                                                                                                                                                                                                                TGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCAAGGGCGA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgess, N.A. and Southan, C.D.
HEZNMAO Serine Protease
Patent: Ep 0890666-A 1.3-TAN-1999;
SMITHKLINE BEECHAM PLC (GB)
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344 c 344 g
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Gaps: 5
Percent Identity: 83.502
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REFERENCE
AUTHORS
TITLE
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ORGANISM
             alignment_block:
US-10-041-006-7 x E31782
                                                                                 alignment_scores:
Quality:
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PF 09-JUN-1998 JP 1998199425
PR 10-JUN-1998 GB 9712088.5,17-OCT-1997 GB 97308295-1, PR 20-FEB-1998 GB 9803650.2
PI NICOLA ANN BAJESU,HELEN ELIZABETH KURINKENNBIADO, PI C12N15/09, A61X31/70, A61X35/76, A61X38/00, A61X38/00, A61X38/00, PR C C12N15/09, A61X31/70, A61X35/76, A61X39/395, A61X48/00,C07K16/40,C12N5/10,C12P21/02,C12P21/08, PC C12N15/00,A61X37/02,A61X37/02,A61X37/02,C12N5/00 CC Strandedness: Single; CC Topology: Linear; FH Key Location
                                                                                                                                              ORIGIN
                                                                                                                                                          BASE COUNT
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyVal...IleSer 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAACTGAG.TTCCAGCCAACGAAGTTTGGCCGCCAG 1074
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Nicola, A.B.H.H. and Kurinkennbiado, C.D.S.
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                                                        1228.50
4.601
89.899
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/db_xref="taxon:32644"
1 344 c 344 g 19
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CCAAACTGAG.TTCCAGCCAACGAAGTTTGGCCGCCAG
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Align seg 1/1 to: E31782 from: 1 to: 1109
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roLysLeuGlnPheGlnProAlaArgLeuGlyGlyGln 289
                                                      TGTCTTAATCCGTGTGAACGGCCAACAAAACTGGATCCATCGGATCATGC 1037
                                                                                                                            TGGGGTTTAGGCCCTGTTCCATGGGTTATGCTTCAAACAGAACCGCCCAG
                                                                                                                                                             TrpGlyGluGly......CysAlaArgGlnAsnArgProGl 260
                                                                                                                                                                                                      TGTGGTGTTCCATGGGGATTCAGTTCCAACCGACAGGCCCAGGGCAAGGG
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                                                                                                                                                                                                                                                                            TTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCAT
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648 ATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAG

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SOURCE
ORGANISM
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TITLE
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alProPheThrAsnTyrIleLeuProValCysLeuProAspProSerVal 150
                                                                                                              nGlyThrAlaSerSerAlaAspValAlaLeuValGluLeuGluAlaProV 134
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                                                                                                                                                                           CACGNTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCCTGTACCA
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                                                                                                                                                                                                                                                                                                      GCAGTGGGTCCTGACGGNTGCGCACTGNTTCCGCAACACNTCTGAGACGT 447
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Ratio: 4.515
milarity: 87.797
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HE2NW40 Serine Protease
Patent: EP 0890646-A 6 13-JAN-1999;
SMITHKLINE BEECHAM PLC (GB)
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KEYWORDS
SOURCE
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LOCUS E31784
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                                                                                        Strandedness: Single;
CC Topology: Linear;
FH Key
FT Source
FT
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PI NICCLA ANN BAJESU, HELEN ELIZABETH KURINKENNBIADO, PI CHRISTOPHER DONALD SAZAN
PC C12N15/09,A61K31/70,A61K35/76,A61K38/00,A61K38/00,A61K38/00,
PC A61K39/395,
PC A61K39/395,A61K48/00,C07K16/40,C12N5/10,C12P21/02,C12P21/08,
PC C12N15/00,A61K37/02,A61K37/02,A61K37/02,C12N5/00 CC
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Patent: JP 1999098992-A 3 13-APR-1999;
SMITHKLINE BEECHAM CORP PUBLIC LTD CO
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E31784
E31784.1 GI:13026588
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JP 1999098992-A/3
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10-JUN-1997 GB 9712088.5,17-OCT-1997 GB
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                                                                    /organism='Unidentified'
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327 c 338 g
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alignment_block:
US-10-041-006-7 x E31784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 TGGCCTTCACCAATNACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTG 647
                                             233 uValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyVal...IleSerT 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVal 50
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GTGGTGTTCCATGGGGATTCAGTTCCAACCGNCAGGCCCAGGGCAAGGGT 938
                                                                                                                        heGluGluGlyLysLysAspAlaCysLys.GlyAspSerGlyGlyProLe 233
                                                                                                                                                                                                                   PheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGly.P 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTTTGAGACGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAG
                                                                                               TCGAGGAGGCCAAGAAGGATGCCTGCAAGTGGG.....
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US-10-041-006-7 x AK055576
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Align seg 1/1 to: AK055576
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Homo sapiens lung cDNA to mRNA, clone_lib:HLUNG2
clone:HLUNG2000255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1522-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Faa:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, RRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (sites)
Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
                                                                                                                                             Quality: 1147.00
Ratio: 4.799
milarity: 85.357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK055576.1 GI:16550340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2066)
Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluation; clone selection for full insert sequencing: \ensuremath{\mathsf{HRI}} .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                460
                                                                                                                                                                                                                                                                                                                                          /clone="HLUNG2000255"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
      from:
                                                                                                                                                Percent Identity:
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Ö
                                                                                                                                                                                                         Length:
                                                                                                                                                      81.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI 31-OCT-2001 weakly similar
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                                                                                                                                                                                                                       261 lTyrileArgValThrAlaHisHisAsnTrpIleHisArgIleIleProL 278
                                                                                                                                                                                                                                                                                                                                               245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1325 GAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1275 CTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCAGGTGGA 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114 ACATTGTGCAGAGAGAGGTGTGGGGCACGGTGGTGGCCAGAGGAGCCCCA 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1064 TCAACACGCATCACCGCTGCACCTGGCTGTCCTAGAGATGACTCTCGAAG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 alGluLeuGluAlaProValProPheThrAsnTyrIleLeuProValCys 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1225 CCAGCACCTCTGAGACGTCCCTGTACCAGGTCCTGCTGGGGGGCAAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 g.AsnThrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGln 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 rpProTrpGlnValSerIleGlnArgAsnGlySerHisPheCysGlyGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 OArgMetLeuAsnArgMetValGlyGlyGlnAspThrGlnGluGlyGluT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                 ysLeuGlnPheGlnProAlaArgLeuGlyGlyGlnLys 290
                                                                                                                                                                                                                                                                                                                     GlyValIleSerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyVa 261
                                                                                                                                                                                                                                                                                                                                                                                 rGlyTrpGlySerProSerGluGluAspLeuLeuProGluProArgIleL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleLysAsnAs 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCCCGACCCCTCGGTGATCTTTGAGACGGGCATGAACTGCTGGGTCAC
                                                                                                                                                                                                  CTACATCCGTGTCACCGCCCACCACAACTGGATCCATCGGATCATCCCCA 182
                                                                                                                                                                                                                                                                                          GGGGTGATCAGCTGGGGTGAGGGCTGTGCCCCGCCAGAACCGCCCAGGTGT 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCTGTGCGCCGGCTTCGAGGAGGGCCAAGAAGGATGCCTGCAAGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGA 1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProAspProSerValIlePheGluThrGlyMetAsnCysTrpValTh 161
                                                                                                         AACTGCAGTTCCAGCCAGCGAGGTTGGGCGGCCAGAAG 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGCTGGAGCCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGC
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160601 dq

DNA

linear

PRI 29-SEP-2001

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TITLE
JOURNAL
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AUTHORS
TITLE
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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AC093517 from: 1 to: 160601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                 AUTHORS
TITLE
                                                                       100328 GCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCATCCAGCGCA 100279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
55 snGlySerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeu
                                                                                              38 yGlnAspThrGlnGluGlyGluTrpProTrpGlnValSerIleGlnArgA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 160601)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-SEP-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 29, 2001 this sequence version replaced gi:15383806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 160601)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
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3.734
24.495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 24.404
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77		77
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77		77
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77		77
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169		169	
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161 98579	LeuProAspProSerValIlePheGluThrGlyMetAsnCysTrpValTh	145 98628	
144 98629	alGluLeuGluAlaproValproPheThrAsnTyrIleLeuProValCys 	128 98678	
128 98679	USERASnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuV 	111 98728	
111 98729	LeuValGlnProGlyProHisAlaMetTyrAlaArgValArgGlnValGl 	95 98778	
94 98779	g.AsnThrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGln   :::	78 98828	
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98879		98928	
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173 98178	ProGluProArgIleLeuGlnLysLeuAlaValProIleIleAspThrPr 189 	9 129
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226		J1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97278 TGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGTGATCAGCTGGGGTGA 97229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97328 TGACGGTGACTCTGCGTCCCCCGCAGGGGGACTCGGGCCGCCCCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97528 CACAAGAAACTGCATTTTCAACACACACACACCCTAGTTGATCTGGGG 97479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97478 ACACTAAAGAATAGGCACTTTAGACAATCGGACTGGCAGGGGATGGGGAG 97429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 isHisAsnTrpIleHisArgIleIleProLysLeuGlnPheGlnProAla 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 CysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGl 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......GlyAspSerGlyGlyProLeuVal 234
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                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 23, 2001 this sequence version replaced g1:14522963. Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 208529)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 16
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Homo sapiens chromosome 16 clone CTD-2270P14, WORKING DRAFT
SEQUENCE, 2 ordered pieces.
                                                                                                                                                               Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the genBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                          This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
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TOSSOR	103400 ABAABCBBCCCCBBCACBBCTCTBCCCACCBBCCCCTCCTBGCCTTTCCCCA
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105459	105410 GACCCCCTCCATCCCCTCCACCCACTCACCCACTCCCTGTGGGGTCCCTGC
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105409	105360 CAGTTGCAACCGCTGCTCCCGCCGCGGGAGGTGCCTCGCACCGCCCCC
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ers	14" g
	source 1.
jth th.	154083 bp known leng 54346 bp
	provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is ava the accession number will be preserved.

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Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,G., Saunders,E., Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O., Campbell,G., Fawcett,J., Maltble,M., Misra,M. and Deaven,L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D., Jones,M., Bucklagham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M., Misra,M. and Deaven,L.

Sequencing of Human Chromosome 16p13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JAN-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 40179)
Ricke,D.O. and Wagner,R.P.
Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 16, cosmid clone 400D1 (LANL), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40179)
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AC004036.1 GI:2811104
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complement/for?
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                                                                                                                                               "Alu"
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alignment_block:
US-10-041-006-7 x AC004036
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ORIGIN
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Ratio: 3.711
Percent Similarity: 24.404
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20020 CGACCCCTCCATCCCCTCCACCCACTCACCCACTCCCTGTGGGTCCCTG 20069
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                                                                                                                                                   19920 GCCCCTCCCACCCAGATGCTTCCCTTAGGTCCAACTCCAGGGCCTAACTTC 19969
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Gaps: 4
Percent Identity: 24.404
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20369	) CACCTCACACCTCAACACCGCAGCTCTAATTATTTTAAACCCCCACATCTT	20320
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JOURNAL
REFERENCE
AUTHORS
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Peters, L., Peters, L., Peters
                                         Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tanje, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Pan troglodytes clone RP43-45G20,
                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimpanzee
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                                                                                                                                                                                                                                                                                                                (bases
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                            1 to 199706)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tamerisa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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REFERENCE

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ACCESSION

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Align seg 1/1 to: AC097329
                                                                                                                                                                                                                                                                                                                                                                                   US-10-041-006-7 x AC097329
4988 GCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCATCCAGCGCA 5037
                                                                                                                                                  4938 GCTCCCCCAGCCTGTGGTCGCCCCAGGATGCTGAACCGAATGGTGGGCGG
                                   38 yGlnAspThrGlnGluGlyGluTrpProTrpGlnValSerIleGlnArgA 55
                                                                                                                                                                                             22 AlaAlaThrAlaCysGlyArgProArgMetLeuAsnArgMetValGlyGl 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_da NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * the contigs are represented * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the exact sizes of the gaps are unknown. * This record will be updated with the exact sizes of the gaps are unknown. * This record will be updated with the exact sizes of the gaps are unknown. * This record will be updated with the exact sizes of the gaps are unknown. * This record will be updated with the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47801 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990329
Consensus quality: 195498 bases at least Q40
Consensus quality: 201324 bases at least Q30
Consensus quality: 206344 bases at least Q20
Estimated insert size: 207444; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: ZUAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169440
169540
182345
182445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; M77789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: RP43-45G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM
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3.589
24.334
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP43-45G20"
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47728: gap of unknown length
102375: contig of 54647 bp in length
102475: gap of unknown length
115011: contig of 12336 bp in length
115111: gap of unknown length
115111: gap of unknown length
139605: contig of 24494 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169539: gap of unknown length
182344: contig of 12805 bp in length
182444: gap of unknown length
190235: contig of 7791 bp in length
190335: gap of unknown length
190663: contig of 6328 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196763: gap of unknown
199706: contig of 2943
                                                                                                                                                                                                                                                                                                    from: 1 to: 199706
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í		77
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5487	TCCCGCACACACCTCAGCTCCAGGACACTCTTCCCGGGAGGAACTCTGCT	5438
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5287	GCCCCTCCCACCCAGATGCTTCCCTTAGGTCCAACTCCAGGGCTAACTTC	238
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5187	CATAGCGCTGACAGCGCCCCGCGCGCTACCGGTTCAGCACCGTGGACAGC	5138
77		77
77 5137	ThralaalaHisCysPhe	72 5088
5087	ACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCCTG	5038
:	SnGlvSerHisPheCvsGlvGlvSerLeuTlealaGluGlamanvallou	55

169		169
6837	GATGTGCCTCAAGAAGGCCCAGGACGGCTTGGGGACCACTCTGAACCCAC	6788
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169 6787	pGlySerProSerGluGlu	163 6738
163 6737	AspProSerValIlePheGluThrGlyMetAsnCysTrpValThrGlyTr 	147 6688
146 6687	euGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuPro 	130 6638
130 6637	nProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuValGluL                   CCCCCTGTACCAGGGCATGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGC	113 6588
113 6587	GlnProGlyProHisAlaMetTyrAlaArgValArgGlnValGluSerAs 	97 6538
96 6537	hrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuVal 	80 6488
	CCCCACACGAGGGGCCCCCCCCACCACCACCACCACCACC	6438
80	CAGTGGTGGCCAGAGGAGTCCCCGCCCTCCCGGGCCTG	78
7		2 7
6387	TGCACCTGGCTGTCCTAGAGATGGCTCTCGAAGACACTGTGCAGAGAGAG	6338
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6187	CTGGCCCTGCTGCACCTGGAGGGTTGTTCTCTCCGAGCCAGCC	6138
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7587	TACTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGGGCGCCTGTAGTC	7538
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7387	GCCCAGGGCAGGGTGGGATCATGCCCCGCTCCATGGGCTATGCATTCAAC	7338
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	CGATGTGGTGTCCATGGGGACTCAGTCCTCACCGCCAG	œ
226	sLyss	225
225 7287	eLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaC 	208 7238
208 7237	AsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIl	192 7188
191 7187	roArgIleLeuGlnLysLeuAlaValProIleIleAspThrProLysCys	175 7138
	ACCTCCTGCCCGAAC	7088
7 0	Clighten broglin	<b>7</b> 0
169 7087		<b>,</b> ,
0	CTGCCCCACAGTGCCCTAAGCCAGAGATGGTCTAAACATGAGGAGACGAC	æ
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6987	GAGAGGGGACAGAAAGGGCCCCAGCCTGCTGCCTGGAAGGAGGGAG	6938
169		169
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169		169
000	AATCTTCC1GTTGCTATATTAATACATACACGGTCTCTGTTCACACAG	8589

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REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pat:AX001347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AX001347
                                                                          alignment_block:
US-10-041-006-7 x AX001347
                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                      FEATURES
                                            Align seg 1/1 to: AX001347 from: 1 to: 683
                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 euValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGluGly 252
78 ArgAsnThrSerGluThrSerLeu.TyrGlnValLeuLeuGlyAlaArgG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3 from Patent EP0890646.
                                                                                                                                                                                                                                                                                      1 (bases 1 to 683)
Burgess,N.A. and Southan,C.D.
HE2NW40 Serine Protease
Patent: EP 0890646-A 3 13-JAN-1999;
SMITHKLINE BEECHAM PLC (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                unidentified.
unidentified
                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                             AX001347.1 GI:7241523
                                                                                                                                                                                                                                                                                                                                                                                 unclassified.
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                                                                                                                                                                                                                             /organism="unidentified"
/db_xref="taxon:32644"
205 c 195 g 11
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                                                                                                                     810.50
4.243
86.818
                                                                                                                        Gaps: 7
Percent Identity: 79.091
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REFERENCE
AUTHORS
TITLE
                                                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
                                     COMMENT
                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS E31783
                                                                                                                                                                                                                                                                                      seq_name: gb_pat:E31783
                                                                                                                                                                            KEYWORDS
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E 1 (bases 1 to 683)

IS Nicola,A.B.H.H. and Kurinkennbiado,C.D.S...

Novel compound

Patent: JP 199098992-A 2 13-APR-1999;

SMITHKLINE BEECHAM CORP PUBLIC LTD CO

SMITHGENTIFIED

PN JP 199098992-A/2

PD 13-APR-1999
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                                                                                                                                               unidentified
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                                                                                                                                            160 lThrGlyTrpGlySerProSerGluGluAspLeuLeuProGluProArgI 177
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PR 10-JUN-1997 GB 9712088.5,17-OCT-1997 GB 97308295-1, PR
10-JUN-1997 GB 9712088.5,17-OCT-1997 GB 97308295-1, PR
20-FEB-1998 GB 9803650,2

PI NICOLA ANN BAJESU, HELEN ELIZABETH KURINKENNBIADO, PI
CHRISTOPHER DONALD SAZAN
CC (12N15/09,A61K31/70,A61K35/76,A61K38/00,A61K38/00,A61K38/00,
PC (12N15/09,A61K31/70,A61K35/76,A61K38/00,C12P21/02,C12P21/08,
PC (A61K39/395,A61K48/00,C07K16/40,C12N5/10,C12P21/02,C12P21/08,
PC (212N15/00,A61K37/02,A61K37/02,A61K37/02,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key

CT Topology: Linear;
FH Source

1. 683

FT Source

/Organism-'Unidentified'.
                                                                               euValGluLeuGluAlaProValProPheThrAsnTyrIleLeuProVal
                                                .GlyAspSerGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuG
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Location/Qualifiers
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/db_xref="taxon:32644"
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alignment_block:
US-10-041-006-7 x AB010779
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AUTHORS
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                                                       Percent Similarity:
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                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-JAN-1998) Nozomi Yamaguchi, Institute for Geri Submitted (27-JAN-1998) Nozomi Yamaguchi, Institute for Geri Kyoto Prefectural University of Medicine, Department of Cell Biology; Kajii-cho 465, Kamigyo-ku, Kawaramati Hirokoji, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5948(ex.5848), Fax:81-75-251-5948)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1306)
Yamaguchi, N. and Mitsui, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens hBSSP-4 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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SVLLGAWOLGNPGSRSQKVGVAMVEPHPVYSWKEGACADIALVELERSIQPSERVLPI
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SLSAHRSWYEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"
432 c 402 g 253 t
                                                   739.00
3.421
75.789
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                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                      /note="prosemin"
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hBSSP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="hBSSP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tissue_type="brain"
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56 GlySerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh 72
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                                                                                                                                                                  CTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGT 127
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Ratio:
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Submitted (14-NOV-2000) Rheumatology, Immunology and Allergy,
Brigham and Women's Hospital, Harvard Medical School, 1 Jimmy Fund
Way, Boston, MA 02115, USA
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11602603
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SLSAHRSWVEKLYQGVQLRGRAQGGGALRAPSQGSGAAARS"
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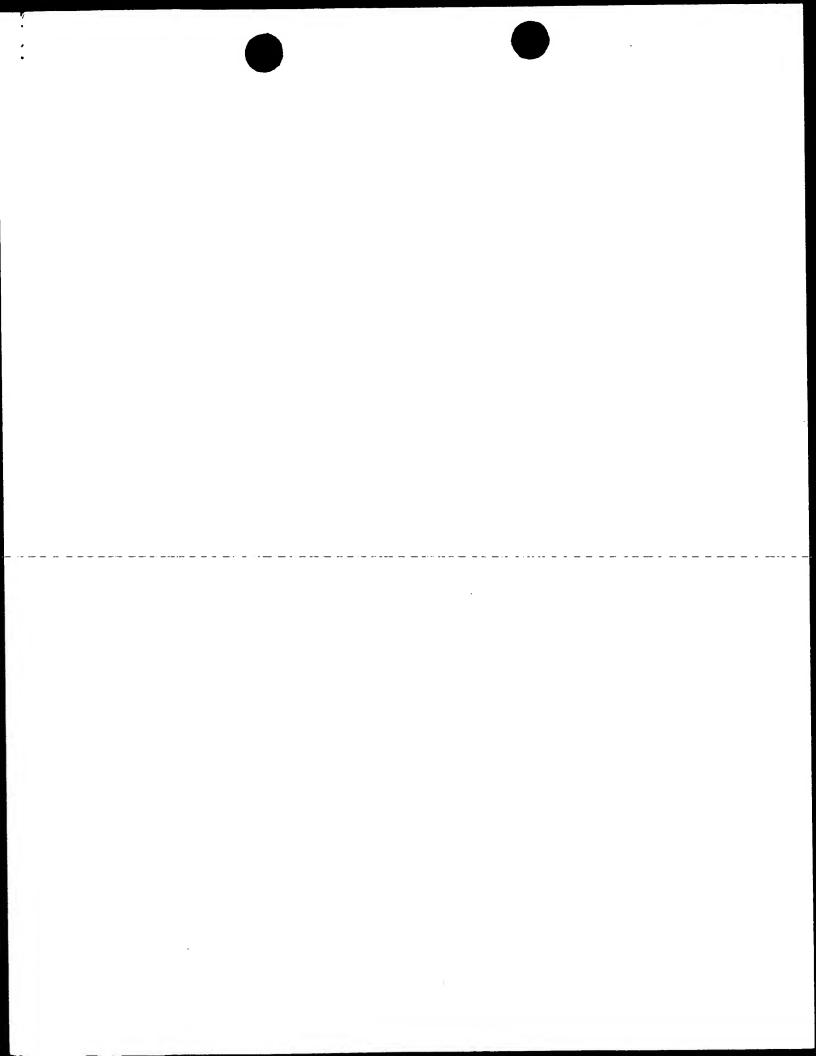
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1403)
                                                                                    human.
                                                                                                                                                                                                Homo sapiens, protease,
                                                               Homo sapiens
                                                                                                                                                                             mRNA, complete cds.
                                                                                                                                   BC009726.1 GI:16307274
                                                                                                                                                                                                   serine,
                                                                                                                                                                                                                     1403 bp
                                                                                                                                                                                                   22,
                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                nRNA linear PRI 22-OCT-2001 clone MGC:9599 IMAGE:3899480,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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REMARK
COMMENT
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: BC009726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-041-006-7 x BC009726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                  199
                                                                                                                                                                                         149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nent_scores:
                                                                                                                                                                                                                                               22
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                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                            TCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTTGTGGGCGGCG
                                                                                                                                                                                                                                                                                                     CTGCTGCTGCCGCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGT
                                                                                                                                                                                                                                                                                                                                                         LeuLeuLeuCys......PheGlySerGlnArgAlaLysAl 22
                         GlySerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh
                                                                                     AGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCATCCAGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: 1 Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 11545838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (29-JUN-2001) National Institutes of Health, Mammalian Submitted (29-JUN-2001) Cancer Gene Collection (MGC), Cancer Genemics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="protease, serine, 22"
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SLSAHRSWYEKIYQGYQLLGRAAQGGGALRAPSQGSGAAARS"

SLSAHRSWYEKIYQGYQLLGRAAQGGGALRAPSQGSGAAARS"

266 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  739.00
3.421
75.789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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Percent Identity:
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349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        887 CTGGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGG
                                                                                                                               270
                                                                                                                                                                          837
                                                                                                                                                                                            254 AlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHisAs
                                                                                                                                                                                                                                                           787
                                                                                                                                                                                                                                                                                                                                               737
                                                                                                                                                                                                                                                                                                                                                                                        220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 GlnProLysThrIleLysAsnAspMetLeuCysAlaGlyPheGluGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 TCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCCTATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 pLeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 CCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 TGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCCATACAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 aSerSerAlaAspValAlaLeuValGluLeuGluAlaProValProPheT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AlaArgValArgGlnValGluSerAsnProLeuTyrGln...GlyThrAl 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 GGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATCAC
937 GGGGT 941
                                        287 lyGly 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 rAlaAlaHisCysPheArg...AsnThrSerGluThrSerLeuTyrGlnV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTGCTGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAG
                                                                                                                                                                                                                                                                                         alG1yG1nSerTrpLeuG1nAlaG1yValI1eSerTrpG1yG1uG1yCys
                                                                                                                                                                                                                                                                                                                                                                                 yLysLysAspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyr 203
                                                                                                                            nTrpIleHisArgIleIleProLysLeuGlnPheGlnProAlaArgLeuG
                                                                                                                                                                     GCCGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTC
                                                                                                                                                                                                                                                                                                                                               GGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCCTCATGTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGGACAGGGA...
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score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query length: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM of: US-10-041-006-7 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-10-041-006-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10041006/runat_13082002_083953_11285/app_query.fasta_1.350
-DB=N_Geneseq_032802 -QFMT=fastap -SUFFIX=p2n.rng -GAPOP=12.000
-GAPDEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPDEXT=4.000 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cd1 -LIST=45 -DOCALICN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=-LOCAL -OUTFWT=pfs
-W=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-US10041006_CGCN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
FIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Results were produced by the GenCore Copyr1ght (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (sec):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         out_format : pfs
                                                                                                                                      9 2.4e-61
9 2.4e-61
4 2e-57
7 1.4e-56
7 9e-56
1.3e-53
4 3.2e-53
9.5e-53
                                                                                                                                                                                                                                                          1 6.6e-62
3 6.9e-62
7 7.0e-62
1.5e-61
                                                                                                                                                                                                                                                                                                               6.6e-62
6.6e-62
                                                         8.2e-50
1.7e-49
                                                                                  4.1e-50
4.2e-50
2.6e-49
                                                                                                                                                                                                                                                                                                                                                                                                           2.5e-109
1.3e-103
                                                                                                                                                                                                                                                                                                                                                      6.4e-62
6.4e-62
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2.1e-142
2.2e-142
                                                                                                                         1.9e-51
6.8e-51
                                                                                                                                                                                                                                                                                                                                                                                .3e-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-123
                                                                                                                                    alignment_block:
US-10-041-006-7 x AAF76994
                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                        Align seg 1/1 to: AAF76994 from: 1 to: 1110
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Sequence 1110 BP; 212 A; 369 C;

335 G; 194 T; 0 other;

Quality:

1571.00 5.417 100.000

Percent Identity:

100.000

17 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34

TCAGAGGGCCAAGGCAACAGCCTGTGGTCGCCCCAGGATGCTGAACC

1 MetArgArgProAlaAlaValProLeuLeuLeuLeuLeuCysPheGlySe 17

ATGAGGCGGCGGCGGTGCCGCTCCTGCTGCTGTTTTTGGGTC

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seq_documentation_block:
ID AAF76994 standard; (XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD03444 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV44326 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV44330 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV42712 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAF21077 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF76994
                                              The present sequence encodes protease T protein. The protein is useful for treating a condition mediated by protease T. It is useful for treating an imbalance of desquamation, by topical application of a pharmaceutical composition containing the protease. The composition is useful as a topical skin care composition. It is useful as a laundry detergent, shampoo, hard surface cleaning composition, and dish care cleaning composition. Protease T protein is useful for treating and preventing skin flaking. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a non-natural
                                                                                                                                                                                                                                              Claim 2; Fig 1; 83pp; English.
                                                                                                                                                                                                                                                                                  New serine protease termed protease T, useful for treating preventing skin flaking or imbalance of desquamation -
                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB73945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protease T; serine protease; dermatological; desquamation; skin care; laundry; detergent; shampoo; skin flaking; ss.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-265889/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2000; 2000WO-US23823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protease T cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0386653.
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594.00 1011.05

588.50 1002.30

588.50 1002.30

588.50 1002.16
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                                                              aHisHisAsnTrpIleHisArgIleIleProLysLeuGlnPheGlnProA
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CGAGGTTGGGCGGCCAGAAG
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS21354

Ĥ seq\_documentation\_block: AAS21354 standard; CDNA; 1129 BP

g×8% AAS21354;

24-OCT-2001 (first entry)

> Human cDNA sequence encoding for PRO4327 polypeptide

numan secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal mus adipocyte; A-peptide; factor VIIA; gene therapy; ss.

Homo sapiens.

07-JUN-2001

01-DEC-1999 01-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 09-DEC-1999 16-DEC-1999 20-DEC-1999 20-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 01-DEC-2000; 2000WO-US32678. 99WO-US28565. 99US-0170262. 99WO-US30095. 99WO-US30999. 99WO-US31243. 99WO-US28564. 99WO-US28634. 99WO-US28551. 99WO-US30911.

18-FEB-2000)
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20-MAR-2000)
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31-MAR-2000)
17-MAY-2000)
17-MAY-2000) 11-FEB-2000 2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
2000WO-US04341.
2000WO-US04414.
2000WO-US04414.
2000WO-US04914.
2000WO-US05601.
2000WO-US05601.
2000WO-US05601.
2000WO-US056037377.
2000WO-US07377.
2000WO-US07377. 2000WO-US15264 2000WO-US30873 2000WO-US14941.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, F Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood Wood WI, Filvaroff E, Sherwood S; Gao

P-PSDB; 2001-408281/43. AAU12282.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical

Claim 3; Fig 221; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cells sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood

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alignment_scores:
Quality:
Ratio:
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10-041-006-7 x AAS21354
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PheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGlyPh
                                                      alProPheThrAsnTyrIleLeuProValCysLeuProAspProSerVal 150
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TTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTT

Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition

is

WPI; 2001-343795/36

Komatsoulis

Birse CE,

Moore

P-PSDB; AAE03821.

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seq_documentation_block:
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                                                                                                                                                               15-NOV-2000; 2000WO-US31282.
19-NOV-1999; 99US-0166414.
21-JUL-2000; 2000US-0219665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzhelmer's disease; food additive; anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; call culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; proliferative disorder; cancer; tumour; asthma foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
                                                                                                                                                                                                                                                                                                                                        mat_peptide
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                                                                                                                                                                                                                                                                                                         "Mature human secreted protein"
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Claim 1; Page 440-441; 553pp; English.

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US-10-041-006-7 x AAD08286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1571.00
Ratio: 5.417
Percent Similarity: 100.000
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                          HisAlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuTyrGl
                                                                                                                                         erLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuValGlnProGlyPro 100
                                                                                                                                                                                                                                                        uGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrS
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CACGCTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCCTGTACCA
                                                                                                               CCCTGTACCAGGTCCTGCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCA
                                                                                                                                                                                                                                                                                                                                          AGCATCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGA
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seq_documentation_block:
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                            05-MAY-1998;
07-AUG-1998;
02-OCT-1998;
                                                                                                                                                                                                          HTRM; human transcriptional regulatory molecule; arteriosclerosis; ALDS arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; ss; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 GAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGC
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                                                                                        04-MAY-1999;
                                                                                                                                                  WO9957144-A2
                                                                                                                                                                              Homo sapiens
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                            98US-0095827.
98US-0102745.
                                                                                       99WO-US09935.
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenocarcinoma and leukaemia; immune disorders such as AIDS, Addison's disease, diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, and myasthemia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques. Polynucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies which specifically bind HTRN and polynucleotides encoding HTRN are useful for diagnosing disorders associated with the expression of HTRN, particularly in assays that detect the expression of HTRN. Nucleotide sequences encoding HTRN may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect differences in gene sequences among normal, carrier and affected individuals. Using diagnostic assays, cancer can be detected prior to the appearance of clinical symptoms and thereby progression of cancer can be prevented by aggressive treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell proliferative disorders such as arteriosclerosis and cirrhosis; cancers including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ52410-Z52474 are human transcriptional regulator molecule (HTRM) nucleotide sequences. The HTRM protein and nucleotide sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 190; 193pp; English
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Gerstin EH,
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84 erLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuValGlnProGlyPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
                                                                                                                                                                                               SerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGl
                                                                               uGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrS 84
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Patterson
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Baughn MR, 1
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Lu DAM;
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seq_documentation_block:
ID AAI58544 standard;
X P X S X K K K K K X E X T X A C
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                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukacenta; se
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                                                        Homo sapiens.
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alignment_scores:
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                                                                                                                                                                                                                                                      US-10-041-006-7 x AAI58544
                                                                                                                                                                                                                                                                      nment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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09-JUL-2000;
19-JUL-2000;
  285
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Wang
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1212 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                         Note:
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19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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                              51
                                                                    34 rgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVal 50
                                                                                                                         17 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
                                                                                                                                                                                                                                                                                              Ratio:
ent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Movel nucleic acids and polypeptides, useful such as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                   .N.S disorders.
ote: The sequence data for this patent did not form part of
MetArgArgProAlaAlaValProLeuLeuLeuLeuLeuCysPheGlySe
                                                                                                              TCAGAGGGCCAAGGCAACAGCCTGTGGTCGCCCCAGGATGCTGAACC
                                                                                                                                                                     ATGAGGCGGCCGGCGGTGCCGCTCCTGCTGCTGCTGTTTTGGGTC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-442253/47
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Ratio: 5.397
milarity: 100.000
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Wang Z,
Zhou P,
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2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0653450.
2000US-0693036.
2000US-0693036.
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Wehrman T, X
, Goodrich R,
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Percent Identity:
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Xu C,
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Xu C, Xue AJ,
Drmanac RT;
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99.655
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                                                                 aH1sH1sAsnTrpIleHisArgIleIleProLysLeuGlnPheGlnProA
                                                                                                                       GluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAl
                                                                                                                                                                            alCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGly
                                                                                                                                                                                                                 rollelleAspThrProLysCysAsnLeuLeuTyrSerLysAspThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisAlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuTyrGl
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                           laArgLeuGlyGlyGlnLys
                                                      GAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGC
                                                                                                                                                               TGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGCTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                   TGAGGAAGACCTCCTGCCGAACCGCGGATCCTGCAGAAACTCGCTGTGC
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CGAGGTTGGGCGGCCAGAAG
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1004
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI60330

seq\_documentation\_block: AAI60330 standard; cDNA; 1157

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4319.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

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alignment_scores:
Quality: 1522.00
Ratio: 5.285
                                                                                                                                                                                                                                                alignment_block:
US-10-041-006-7 x AAI60330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC immunosuppressant and cytostatic activity. The polynucleotide or of the invention may be used to treat diseases of the peripheral nervous System, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity such as: Immune system suppression, CC and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed head of the control of the printed activity.
                                                                                                                                                                                                                 Align seg 1/1 to: AAI60330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-CCT-2000; 2000US-0662191.

19-CCT-2000; 2000US-0727344.
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Wang J,
Zhao QA,
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                                                                                     17 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
                34 rgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVal 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   pecification.
                                                                                                                                                           1 MetArgArgProAlaAlaValProLeuLeuLeuLeuLeuCysPheGlySe
TCAGAGGGCCAAGGCAACAGCCTGTGGTCGCCCCAGGATGCTGAACC
                                                                                                                                          ATGAGGCGGCGGCGGGTGCCGCTCCTGCTGCTGCTGTTTTTGGGTC
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Wehrman T, X
, Goodrich R,
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                                                                                                                                                                                                                                                                                                     Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                             204 T; 0 other;
                                                                                                                                                                                                                                                                                                       98.288
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Yang Y,
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07-JAN-1999

(first entry)

Serine protease; regulation; cell activity; viability; HELA2; ATC2;

Nucleotide sequence of SP003LA, a homologue of HELA2.

seq\_documentation\_block:
ID AAV59136 standard; DNA;

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59136

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940
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ValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGl
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                                                                      CCCACCACAACTGGATCCATCGGATCATCCCCAAACTGCAAGTCCAACCC
                                                                                                                                           TGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCG
                                                                                                                                                             yGluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrA
                                                                                                                                                                                                               GTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGGGGGGGTGATCAGCTGGGG
                                                                                                                                                                                                                                                                                      heGluGluGlyLysLysAspAlaCysLysGlyAspSerGlyGlyProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                               CCATCATCGACACACTCAAGGTGCAACCTGCTCTACAGCAAAGACACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGGAAGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGC
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alignment_block:
US-10-041-006-7 x AAV59136
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                                                                                                                                                                                          Align seg 1/1 to: AAV59136
                                                                                                                                                                                                                                                                                      Quality: 1449.00
Ratio: 5.468
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          testicular germ cell cancers (seminoma) and is also expressed in some non-testicular cancers (of colon, pancreas, prostate and ovary), so is a marker/potential therapeutic target for cancer. The promoter from the HELA2 gene is useful for testis-specific expression of other genes, e.g. for gene therapy or modulation of fertility. Drugs that block activity of HELA2 should have antitumour activity to ther than in testis recombinant HELA2 should stop growth of tumours and normalise sperm development (eliminating the need for orchidectomy). Identification of mutant forms of HELA2 can be used to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV59134-36 represent HELA2 homologues. The genes are found in a cluster on chromosome 16p13.3. HELA2 was isolated from HeLa cells, and has homology to serine proteases. The crotetin is involved in or associated with regulation of cell activity and/or viability. Administration of recombinant HELA2 (also called testisin) is used to increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is also a suppressor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1997;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCOM3; testisin; fertility; suppressor; testicular germ cell cancer; seminoma; testis-specific expression; antitumour; sperm development; infertility; human; chromosome 16p13.3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 980 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New serine protease(s) and kinase involved in regulating cell activity and viability - particularly the testis-specific protease HELA2 used for modulation of fertility and as tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 15; Fig 20C; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW77304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-480768/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antalis TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
.59
                                        53
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                                                                                                                  w
                                                                                                                                  CysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrGl 42
                                                        nGluGlyGluTrpProTrpGlnValSerIleGlnArgAsnGlySerHisP 59
                                                                                                                  heCysGlyGlySerLeuIleAlaGluGlnTrpValLeuThrAlaAlaHis
                                        GGAGGGCGAGTGGCCTGGCAAGTCAGCATCCAGCGCAACGGAAGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-0000422.
97AU-0005101.
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/product= SP003LA
/note= "sequence /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
3..899
                                                                                                                                                                                                                                                                                                                                                                                                      192 A;
                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                        Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                        289 G; 174 T;
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                                                                                                                                                                                            980
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                                        102
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seq_documentation_block:
ID AAF77000 standard; cI
XX
AAF77000;
XX
APF77000;
XX
29-MAY-2001 (first e
XX
DE Fusion gene of protea
XX
Human; protease T; se
KW Human; protease T; se
KW skin care; laundry; c
KW zymogen activation ve
XX
OS Homo sapiens.
OS Synthetic.
                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF77000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 lnValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspVal 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 IleProLysLeuGlnPheGlnProAlaArgLeuGlyGlyGlnLys 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                    703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 nLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 CGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 rpValThrGlyTrpGlySerProSerGluGluAspLeuLeuProGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 oValCysLeuProAspProSerValIlePheGluThrGlyMetAsnCysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCTGCTGGGGGC
                                                                                                                Human; protease T; serine protease; dermatological; desquamation;
                                                                                                                                                          Fusion gene of protease T in a zymogen activation vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 uGlnAlaGlyVallleSerTrpGlyGluGlyCysAlaArgGlnAsnArgF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 LysGlyAspSerGlyGlyProLeuValCysLeuValGlyGlnSerTrpLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AlaLeuValGluLeuGluAlaProValProPheThrAsnTyrIleLeuPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 AAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGC
                                                                                                                                                                                                                                                                                                                                                                       753 ATCCCCAAACTGCAGTTCCAGCCAGCGAGGTTGGGCGGCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 aArgGlnLeuValGlnProGlyProHisAlaMetTyrAlaArgValArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGTGTCTACATCCGTGTCACCGCCCACCACAACTGGATCCATCGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roGlyValTyrIleArgValThrAlaHisHisAsnTrpIleHisArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGGCGGGGTGATCAGCTGGGGGTGAGGGCTGTGCCCGCCAGAACCGCC
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                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                             CDNA; 1130
                                                                                detergent; shampoo;
vector; ss.
                                                                                                                                                                                                                                                                             ВP
                                                                                                  flaking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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alignment_block:
US-10-041-006-7 x AAF77000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PN XXX PPR XXX PPR XXX PPR XXX PPR XXX PPR XXX PPR DR X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAF77000
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a protease T fusion protein. Protease T is useful for treating a condition mediated by protease T. It is useful for treating an imbalance of desquamation, by topical application of a pharmaceutical composition containing the protease. The composition is useful as a topical skin care composition. It is useful as a laundry detergent, shampoo, hard surface cleaning composition, and dish care cleaning composition. Protease T protein is useful for treating and preventing skin flaking. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a non-natural
                                                                                                                                                                                                                     410
                                                                                                                                                                                                                                                                                                                                                                 360
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149 rValilePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1130 BP; 249 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          environment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 laGluGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 AsnArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 GACAAGATCGTTGGGGGCTATGCTCTAGAGGAGGGCGAGTGGCCCTGGCA 209
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                                                                                                              ProValProPheThrAsnTyrIleLeuProValCysLeuProAspProSe 149
                                                                                                                                                                                                          yProHisAlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuT 116
                                                                         ACCACACGCTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGAGCAGTGGGTCCTGACGGCTGCGCACTCCTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCAGCATCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCG
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Ratio: 5.384
milarity: 98.837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0386653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
0
97.287
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seq_documentation_block:
ID AAX06942 standard; cD
XX AAX06942;
AC AAX06942;
XY 10-MAY-1999 (first e
XX 10-MAY-1999 (first e
XX Erine protease HEZNW
XX HEZNW40; serine prote
KW HEZNW40; serine prote
KW wasting disease; athe
neurodegenerative dis
KW therapy; vaccine; ss.
XX Homo sapiens.
Y**
FT CDS 197: 197: 7**
FT CDS 197: 7**
FT CDS 7**
FT CDS 7**
FT CDS 98EP-0
XX EP890646-A2.
XX EP890646-A2.
XX 20-FEB-1998; 98EP-0
PR 10-JUN-1997; 97GB-0
PR 10-JUN-1998; 98GB-0
PR 10-JUN-1998; 9
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                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM PLC
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97GB-0012088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tag analysis. HE2NW40 polypeptides and polynucleotides are useful C for diagnosing diseases related to over or underexpression of C HE2NW40 protein by identifying mutations in the HE2NW40 gene, C and/or analysing the presence or amount of expressed polypeptide (claimed). HE2NW40 polypeptides, polynucleotides (gene therapy), C antisense sequences, agonists and antagonists, and soluble polypeptides that bind the HE2NW40 ligand to prevent expression, C can be used to modulate HE2NW40 expression or activity. Diseases of diagnosed, prevented or treated include cancer, inflammation, sthma, wasting diseases, atherosclerosis, stroke, diabetes, rithritis, and neurodegenerative diseases and disorders including Alzheimer's disease. HE2NW40 polynucleotides can also be utilised in the recombinant production of HE2NW40 polypeptides.
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                    134 alProPheThrAsnTyrIleLeuProValCysLeuProAspProSerVal 150
                                                                                     547
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                                                                                                                                                                                                                                                                 uGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrS
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                                                                                                            nGlyThrAlaSerSerAlaAspValAlaLeuValGluLeuGluAlaProV 134
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TGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCAAGGGCGA
                                                                                     GGGCACGGCCTCCAGCGCTTACGTGGCCCCTGGTGGAGCTGGAGGCACCAG
                                                                                                                                                                             CACGCTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCCTGTACCA
                                                                                                                                                                                                                                                                                                                                                         GCAGTGGGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGT 446
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10-JUN-1997;
17-OCT-1997;
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                                                                                                                                                                                                                                                                             HE2NW40; serine protease; human; cancer; inflammation; asthma; wasting disease; atherosclerosis; stroke; diabetes; arthritis; neurodegenerative disease; Alzheimer's disease; diagnosis;
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                                                                                                                                        13-JAN-1999.
                                                                                                                                                               EP890646-A2.
                                                                                                                                                                                                                                         Homo sapiens.
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                                   (SMIK ) SMITHKLINE BEECHAM PLC
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Burgess

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Clinkenbeard HE,

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                                         134
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                                                                                                                                                                                                                                                          erLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuValGlnProGlyPro
                                                                                                nGlyThrAlaSerSerAlaAspValAlaLeuValGluLeuGluAlaProV
                                                                                                                                                         CACGNTATGTATGCCCGGGTGAGGCAGGTGGAGGAGCAACCCCCTGTACCA
                                                                                                                                                                                                                                     CCCTGTACCAGGTCCTGCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCA
                                                                                                                                                                                                                                                                                                                 GCAGTGGGTCCTGACGGNTGCGCACTGNTTCCGCAACACNTCTGAGACGT
                                                                                                                                                                                                                                                                                                                                      uGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrS
                                                                                                                                                                                                                                                                                                                                                                                             ACCATCCAGCGCAACGGAAGCCANTTTTGCGGGGGCAGCTTCATCGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                 SerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAANNGTGGGNNGGCAGGACACGCAGGAGGGCCGAGTGGCCCTGGCAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAGGCGGCCGGCGGTGCCGCTCCTGCTGCTGCTGTTTTNTNNGTN
TGGCCTTCACCAATNACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTG
                                                                           GGCACGCCTTCCAGCGCTGACGTGGCCCCTGGTGGAGCTGGAGGCACCAG
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4.515
87.797
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Percent Identity:
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5
80.678
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seq_documentation_block:
ID AAX06943 standard.
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                                                            20-FEB-1998;
10-JUN-1997;
17-OCT-1997;
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                                                                                                                                                                                                                                                                               HE2NW40; serine protease; human; cancer; inflammation; asthma; wasting disease; atherosclerosis; stroke; diabetes; arthritis; neurodegenerative disease; Alzheimer's disease; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277
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                                                                                                                01-JUN-1998;
                                                                                                                                        13-JAN-1999
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                   Serine protease HE2NW40 homologous EST clone.
                                                                                                                                                                                                                                                                                                                                                              10-MAY-1999
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                                                                                                                                                                                                                                                                   therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGTGTTCCATGGGGATTCAGTTCCAACCGNCAGGCCCAGGGCAAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX06943
                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                            98GB-0003650.
97GB-0012088.
97EP-0308295.
                                                                                                               98EP-0304312
                                                                                                                                                                                                       Location/Qualifiers 72..251
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Burgess NA,

Clinkenbeard HE,

Southan CD;

(SMIK ) SMITHKLINE BEECHAM PLC

P-PSDB;

AAW88454.

WPI; 1999-072882/07

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alignment_block:
US-10-041-006-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has at least 70% identity to this sequence. Such polynucleotides can be obtained from a cDNA library derived from mRNA in cells of human neutrophils, adipose or synovial tissue, using expressed sequence tag analysis. A polynucleotide encoding a serine procease termed HE2NW40 (see W884453) is specifically claimed. HE2NW40 polypeptides and polynucleotides are useful for diagnosing diseases related to over or underexpression of HE2NW40 protein. They can also be used to modulate HE2NW40 activity. Diseases diagnosed, revented or treated include cancer, inflammation, asthma, wasting hiseases, atherosclerosis, stroke, diabetes, arthritis, and neurodegenerative diseases and disorders including Alzheimer's
                                                                            351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New serine protease HE2NW40 polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of cancer, Alzheimer's disease and asthma
                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
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                                                                                                                                                                                                                               lGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAsnThrSerGluThrSerLeu.TyrGlnValLeuLeuGlyAlaArgG
                  nAspMetLeuCysAlaGly.PheGluGluGlyLysLysAspAlaCysLys
                                                                                                LeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleLysAs
                                                                                                                                                                                                                                                                                                                                                CysLeuProAspProSerValIlePheGluThrGlyMetAsnCysTrpVa
                                                                                                                                                                                                                                                                                                                                                                                                          euValGluLeuGluAlaProValProPheThrAsnTyrIleLeuProVal
                                                                                                                                                                           leLeuGlnLysLeuAlaValProIleIleAspThrProLysCysAsnLeu
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TGACATGCTGTGCGCCGGNTTTCGAGGAGGGCAAGAAGGATGCCTGCAAG
                                                                            CTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAAGAA
                                                                                                                                                      TCCTGCAGAAACTCGCTGTGCCCCATCATCGACACCCCAAGTGCAACCTG
                                                                                                                                                                                                                                                                                                             TGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGAACTGCTGGGT
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86.818
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seq_documentation_block:
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                                                                                                                The invention relates to novel serine proteases designated BSSP4 (AABIL700-B11709), and to nucleic acids encoding them (AAA61695-A61704, AAA61799). The invention also relates to vectors and transformants comprising BSSP4 nucleic acids; transgenic animals in which the expression level of BSSP4 can be varied; and an mBSSP4 knockout mouse. The invention additionally encompasses anti-SSP4 antibodies and methods of production of such antibodies, methods of BSSP4 detection using the antibodies, and the use of BSSP4 proteins or fragments as diagnostic markers for certain medical conditions. Nucleotides encoding BSSP4 were not the conditions. Nucleotides encoding BSSP4 were
proteases. The BSSP4 serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland and testis) as diagnostic markers for diseases associated with altered BSSP4
                                                                                                                                                                                                                                                                                                                                                       Serine protease BSSP4 diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initially isolated in a human brain cDNA library using degenerate PCR primers (AAA61714-A61715) based on conserved regions of serine
                                                                                                                                                                                                                                                                                                                  Claim 4; Page 67-69; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-400084/34.
P-PSDB; AAB11701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uemura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; oedema; dropsy; cancer; inflammation; prostate; testis; bone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding human serine protease BSSP4 (hBSSP4) SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA61696 standard; cDNA; 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 CTTCAAACAGAANCGCCCAGTGTCTAAATCCGTGTNAACGGCCAACAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 lnAlaGlyVal...IleSerTrpGlyGluGly......Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 .GlyAspSerGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kominami
                                                                                                                                                                                                                                                                                                                                                         and antibodies recognizing BSSP4 for assay and in which BSSP4 expression is altered -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaguchi
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alignment_block:
US-10-041-006-7 x AAA61696
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gn seg 1/1 to: AAA61696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1007 BP; 171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression levels. Such diseases include Alzheimer's disease, oedema (dropsy), cancer or inflammation of brain, prostate, testis or bone. Sequences AAA61695-A61703 ans AAA61793 represent CDNAs encoding human BSSP4 variants (hBSSP4), and sequence AAA61704 represents CDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164
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                                        TCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCCTATCATCG
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                                                                                                                                                                                                                                                                                                   CCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGT 563
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yLysLysAspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuV
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17-MAR-2000;
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(HUMA-) HUMAN GENOME SCI INC

CA, Barash SC,

WPI; 2001-465566/50. P-PSDB; AAU23215.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous

Claim 4; SEQ ID No 311; 1180pp; English.

CC The present invention relates to the isolation of novel human enzyme CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences cc encoding them. The enzyme polypeptides of the invention may comprise the CC functional classes of oxidoreductases, transferases, hydrolases, lyases, CC isomerases or ligases. The sequences of the invention are useful in the C diagnosis, treatment, prevention and/or prognosis of a wide range of CC disorders including hyperproliferative disorders (e.g. cancer), CC immunodeficiency disorders (e.g. ALDS) autoimmune disorders (c.g. arthritis), neurological disorders (e.g. Alzheimer's disease), CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (c.g. arthritis), cardiovascular disorders (e.g. atherosclerosis), CC blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The CC (e.g. infertility) and infectious disorders (e.g. influenza) in the CC polynucleotides of the invention can also be used in gene therapy. CC AAS40785-AAS41684 represent cDNA sequences encoding for the novel human contains the containers of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1352 B₽; 238 446 Ç 407 G; 261

alignment\_scores:

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P-PSDB; AAU17037.
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2000US-0249217.
2000US-0249218.
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polypeptides and polynucleotides useful as diagnostic reagents lose diseases or disorders associated with aberrant expression or trying polypeptides, for treating blood clotting disorder, or ξ

The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in cliquous combant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders c.g. cardiac arrest, or increase and fungi cand ocular disorders e.g. corneal infection, and many other candocular disorders e.g. corneal infection, and many other cornect skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to capabilities, fat content, lipid, protein, carbohydrate, vitamins, mice. minerals, cofactors and fat content, lip actors and other pid, protein, carbohydrat
nutritional components. The present

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Percent Identity:

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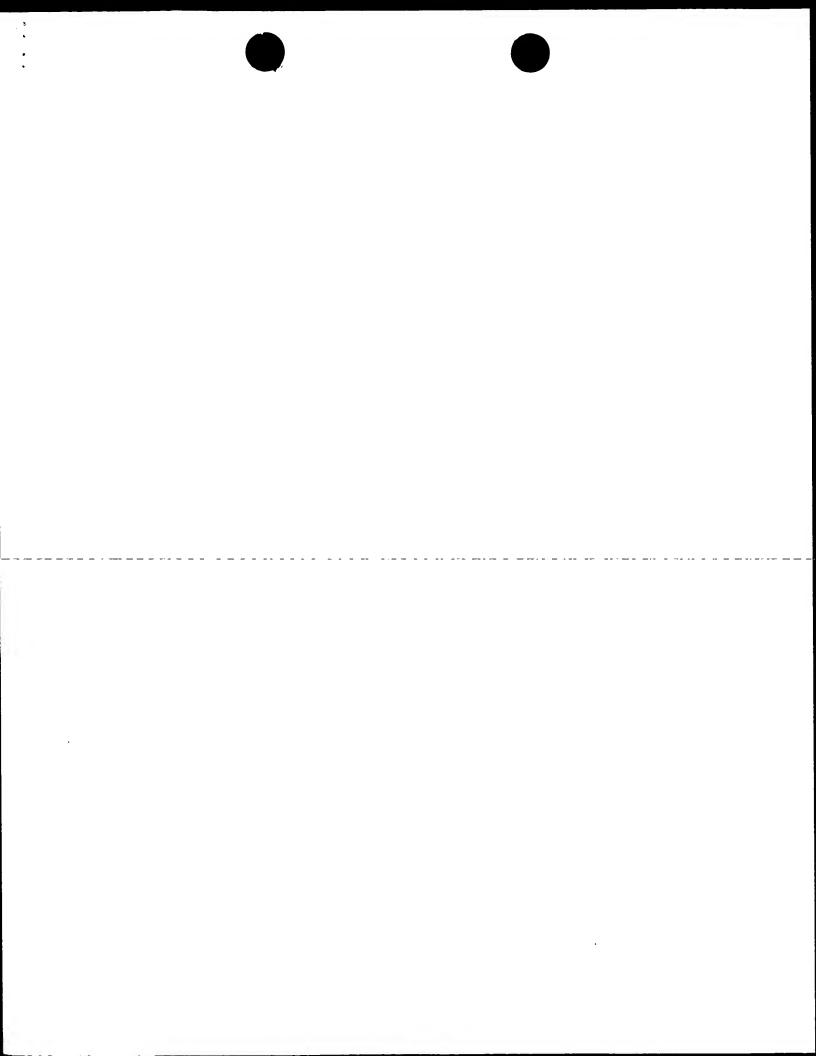
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ID AAX87259 standard:
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                  This is the nucleotide sequence of cDNA clone DNA43318 (ATCC 209481) coding for human PRO343 (UNQ302) (see AAY06482). The clone was isolated from a foetal lung library. Amplification of DNA43318 (chromosome 16) was observed in primary lung and primary colon tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO343 may have utility in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may cat as predictors of the prognosis of tumour treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1998;
05-JAN-1998;
29-APR-1998;
22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO343; UNQ302; cancer; tumour; diagnosis; therapy; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clone encoding human PRO343, amplified in tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1999
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                                                                                                                                                                                                                                       Antibody against proteins expressed tumor diagnosis and treatment
                                                                                                                                                                                                                                                                              P-PSDB; AAY06482
                                                                                                                                                                                                                                                                                             WPI; 1999-430385/36
                                                                                                                                                                                                                                                                                                                                   Botstein D,
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                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                       Wood WI;
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98US-0070440.
98US-0083500.
98US-0086414.
98US-0088742.
98US-0107783.
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149..1003
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alignment_block:
US-10-041-006-7 x AAX87259
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                                                AlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHisAs 270
                                                                                                                                                                       YLYSLYSASPALACYSLYSGLYASPSerGLYGLYProLeuValCysLeuV 237
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                                                                                                                 alGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGluGlyCys 253
                                                                                                                                                           GGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCCTCATGTGCCAGG
                       nTrpIleHisArgIleIleProLysLeuGlnPheGlnProAlaArgLeuG 287
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287 lyGly 288 ||||| 951 GGGGT 955



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CGP12_6/Ptcdata/1/ina/56_COMB.seq:US-09-088-651-1 + 1128.50 2431.94 9, 06-128 1109  
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/cgp12_6/Ptcdata/1/ina/56_COMB.seq:US-09-088-651-3 + 110.50 1100.32 11.9e-81 633 1  
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/cgp12_6/Ptcdata/1/ina/56_COMB.seq:US-09-016-366A-18 + 578.50 1130.20 2.9e-55 1081  
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/cgp12_6/Ptcdata/1/ina/56_COMB.seq:US-09-016-366A-14 + 578.50 1111.41 1 1.5e-54 1154  
/cgp12_6/Ptcdata/1/ina/56_COMB.seq:US-09-016-366A-14 + 565.50 1111.41 1 1.5e-54 1154  
/cgp12_6/Ptcdata/1/ina/56_COMB.seq:US-09-016-366A-14 + 565.50 1103.87 8.5e-54 1108  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
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-Q-/cgn2_1/USPTO_spool/US10041006/runat_13082002_083953_11268/app_query.fasta_1.350
-Q-/cgn2_1/USPTO_spool/US10041006/runat_13082002_083953_11268/app_query.fasta_1.350
-DB-ISSUMC_Patents_NA -QFWTF-fastap -SUFFIX-p2n.rni
-GAPOP=12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-COOPEXT-0.000 -QGAPOP-4.500 -GGAPEXT-0.050 -YGAPOP-10.000
-YGAPEXT-0.500 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-THE_SCORE-pct -THR_MAX-100 -THR_MIN-0 -MINIGN-15 -MODE-LOCAL
-OUTFWT-pfs -NORM-ext -HEAPSIZE-500 -MINIEN-0 -MAXIEN-2000000000
-GGAPEXT-0.500 -GGAPLT-10 -THR_MAX-100 -THR_MIN-0 -MINIEN-0 -MINIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-041-006-7
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seq_documentation_block:
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-008-271A-1B + 465.5
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-807-151-2 + 462.00
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-518-046-1 + 462.00
                                                                                                                            alignment_block:
US-10-041-006-7 x US-09-088-651-1
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                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                         US-09-088-651-1
                                                                                Align seg 1/1 to: US-09-088-651-1 from: 1 to: 1109
                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09088651 Patent No. 6165771
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APPLICATION NUMBER: GB9712088.5

FILING DATE: 10-JUNE-1997

APPLICATION NUMBER: EP 97308295.1

FILING DATE: 17-OCT-1997

APPLICATION NUMBER: GB 9803650.2

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F.

REGISTRATION NUMBER: 23,031

REGISTRATION NUMBER: GB130358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: BURGES
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CLINKENBEARD, HELEN E. APPLICANT: SOUTHAN, CHRISTOPHER D. TITLE OF INVENTION: NOVEL COMPOUNDS
197 ATGAGGCGGCGGCGGCGGTGCCGCCTGCTGCTGCTGTTTTGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09, FILING DATE: JUNE 1, 1998 CLASSIFICATION:
                      1 MetargargProAlaAlaValProLeuLeuLeuLeuLeuCysPheGlySe 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. BOX 98
CITY: VALLEY FORGE
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Ratio: 4.601
milarity: 89.899
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                                                                                                                                                                                          Percent Identity: 83.502
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2.9e-42
9.7e-42
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17 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34

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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-088-651-6
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                                    CCAAACTGAG.TTCCAGCCAACGAAGTTTGGCCGCCAG
                                                                                                                         yValTyrIleArgValThrAlaHisHisAsnTrpIleHisArgIleIleP 277
                                                                                                                                                                                                                                                                                                                                       PheGluGluGlyLysLysAspAlaCysLys.GlyAspSerGlyGlyProL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGl 67
                                                                     roLysLeuGlnPheGlnProAlaArgLeuGlyGlyGln 289
                                                                                                         TGTCTTAATCCGTGTGAACGGCCAACAAAACTGGATCCATCGGATCATGC
                                                                                                                                                                            TGGGGTTTAGGCCCTGTTCCATGGGTTATGCTTCAAACAGAACCGCCCAG
                                                                                                                                                                                                           TrpGlyGluGly......CysAlaArgGlnAsnArgProGl 260
                                                                                                                                                                                                                                                                                  euValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyVal...IleSer 248
                                                                                                                                                                                                                                                                                                                                                                                      TTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCAT 846
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                                                                                                                                                                                                                                                TGTGGTGTTCCATGGGGATTCAGTTCCAACCGACAGGCCCAGGGCAAGGG
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seq\_documentation\_block:

Sequence 6, Application US/09088651 Patent No. 6165771

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                      US-10-041-006-7 x US-09-088-651-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                         348
                                                                                                                 298 NAANNGTGGGNNGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTC
                                                                                                                                                                                                                                                                         198 ATGAGGCGGCGGCGGCGGTGCCGCTCCTGCTGCTGCTGTTTNTNNGTN 247
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FILING DATE: 10-JUNE-1997
APPLICATION NUMBER: EP 97308295.1
FILING DATE: 17-OCT-1997
APPLICATION NUMBER: GB 9803650.2
FILING DATE: 10-OCT-1997
                                                                                                                                                                                             248 TCAGAGGGCCAAGGCAACAGCNTGTGGTCGCCCCAGGATGCTGAACN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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APPLICANT: CLINKENBEARD, HELEN E.
APPLICANT: SOUTHAN, CHRISTOPHER D.
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
67 uGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrS 84
                                                                           51 SerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGl
                                                                                                                                   34 rgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVal
                                                                                                                                                                                                             17 rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: PRESTIA, PAUL F. REGISTRATION NUMBER: 23 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                       AGCATCCAGCGCAACGGAAGCCANTTTTGCGGGGGCAGCTTCATCGCGGA
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Ratio: 4.515
milarity: 87.797
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O. BOX 980
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JUNE 1, 1998
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                                                                                                                                                                                                                                                                   Sequence 3, Application US/09088651
Patent No. 6165771
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 roIleIleAspThrProLysCysAsnLeuLeuTyrSerLysAspThrGlu 200
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                                                                                                                                                           APPLICANT: BURGESS, NICOLA A.
APPLICANT: CLINKENBEARD, HELEN E.
APPLICANT: SOUTHAN, CHRISTOPHER D.
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
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                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                             STREET: P.O. BOX 91
CITY: VALLEY FORGE
                                          COUNTRY:
                                                         STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAG
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USA
19482
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alignment_block:
US-10-041-006-7 x US-09-088-651-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 683 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                           144 CysLeuProAspProSerValIlePheGluThrGlyMetAsnCysTrpVa
                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                            127 euValGluLeuGluAlaProValProPheThrAsnTyrIleLeuProVal 143
                                                                                                                                                                                                                                                                                                                                                     101 GGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCC
                                                                                                                                                                                                                                                                                                                                                                          110 1GluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaL
                                                                                                                 160 lThrGlyTrpGlySerProSerGluGluAspLeuLeuProGluProArgI
194 LeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 lnreuvalGlnPro.GlyProHisalaMetTyrAlaArgValArgGlnVa 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB9712088.5 FILING DATE: 10-JUNE-1997 APPLICATION NUMBER: EP 97308295.: FILING DATE: 17-OCT-1997 APPLICATION NUMBER: GB 9803650.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: JUNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTAGTGCAGCCGGGGACCACACGCTATGTATGCCCCGGGTGAGGCAGGT 100
                                        TCCTGCAGAAACTCGCTGTGCCCATCATCGACACACCCCAAGTGCAACCTG
                                                           leLeuGlnLysLeuAlaValProIleIleAspThrProLysCysAsnLeu
                                                                                                                                                                                             TGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGAACTGCTGGGT
                                                                                                                                                                                                                                                                          TGGTGGAGCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTG
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Ratio:
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86.818
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US-08-978-404B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1219 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                              FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth 1
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 nTrpIleHisArgIleIleProLysLeuGlnPheGlnProAlaArgLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 CTGGATCCATCGGATCATNCCCAAACTGAG.TTCCAGCCAACGAAGTTTG
                                    STRANDEDNESS:
                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US FILING DATE: 25-NOV-97
                 TOPOLOGY:
                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/032,354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHisAs 270
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                 linear
                                  single
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                                                                                                                                                                                                                        B0801/7090
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alignment_block: us-10-041-006-7 \times us-08-978-404B-7
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-978-404B-7
921 GGCTGTGCTCTGCCCAACAGGCCTGGCATCTACACTCGGGTCACCTATTA
                           252 GlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHi 268
                                                                                                         871 GCAAGGTAAACGGTACCTGGCTGCAGGCAGGTGTGGTCAGCTGGGGTGAG
                                                                                                                                                                                                         824 CGAAGGA...CACGACTCCTGCCAGGGTGACTCCGGAGGACCTCTGGTCT
                                                                                                                                                                                                                                                                                                                777 GGGGACAACATCCACATTGTCCGAGACGACATGCTGTGTGCTGGG...AA
                                                                                                                                                                                                                                                                                                                                              202 GlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGlyPheGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 TTCCCCTCAGGAACATTGTGCTGGGTGACAGGCTGGGGAAACATCGACAA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 PheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerG1 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577 ACATTTCCAGCCATGTCCACCCCGTCTCCCTGCCTCCTGCCTCAGAGACC 626
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                                                                                                                                                                                                                                                           218 uGluGlyLysLysAspAlaCysLysGlyAspSerGlyGlyProLeuValC
                                                                                                                                                                                                                                                                                                                                                                                                                         727 TCGTGGAAAACCAGCTTTGTGACCTGAAGTATCACAAAGGTGTCTACACA 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 GGTGCTCACCGCGCACACTGTGTGGGACCGACTATTGCTGATCCCAACA 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 GTGCCAAGAGTGGGGC..
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                                                                                                                            ysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGlu
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335
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seq_documentation_block:
; Sequence 20, Application US/09016366A
; Patent No. 5955431
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                                                                                                                                                                                                                                                                                                    alignment_block:
US-10-041-006-7 x US-09-016-366A-20
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                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-016-366A-20
                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,091
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: B0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                      61
                                                                                                            25 aCysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrG 42
                        42 lnGluGlyGluTrpProTrpGlnValSerIleGlnArgAsnGly..... 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                        9 LeuLeuLeuLeuCysPheGlySerGlnArgAlaLysAlaAlaThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-720-2441
                                                                   CCCAGGCCAGGCCTGCAGCGAGTGGGCATCGTTGGGGGTCAGGAGGCCC 110
                                                                                                                                                               CTGCTGCTGCCGCGTCCTGGCGAGCCGCCCTACGCGGCCCCTGC
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                       588.50
3.147
68.248
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                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
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                                                                                                                                                                                                                                                        from: 1 to: 1128
                                                                                                                                                               60
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seq\_documentation\_block:
; Sequence 15, Application US/08978404B
; Patent No. 5968782

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &

Sacks, P.C.

ADDRESSEE: WOII, CARREET: 600 Atlantic Avenue

STREET: 00.

NUMBER OF SEQUENCES:

seq\_name: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:US-08-978-404B-15

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121 rSerAlaAspValAlaLeuValGluLeuGluAlaProValProPheThrA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 CCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 TGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGAC
                                                                                                                       746 CAGCCCAACCGGCCTGCCATCTACACCCGTGTCACCTACTTGGACTG 795
                                                                                                                                                                                                                                                                                238 lyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGluGlyCysAla 254
                                                                                                                                                                                                                                                                                                                                                                                                              221 sLysAspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuValG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 GTCCGCATCGTCCGTGACGACATGCTGTGCCGGG.....AACACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 uLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAspT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 GCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCCCCCCG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 snTyrIleLeuProValCysLeuProAspProSerValIlePheGluThr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 CGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 CTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AlaArgValArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 TGCAACTGCGGGAGCAGCACCTCTACTAC.....CAGGACCAGCTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 CGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 CCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATAC
                                                                                                                                                                                                                                                  646 GAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 hrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGln 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGluAspLe 171
                                                        271 pIleHisArgIleIleProLys 278
                                                                                                                                                                                      255 ArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHisAsnTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 alLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 rAlaAlaHisCysPhe...ArgAsnThrSerGluThrSerLeuTyrGlnV
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GATCCACCACTATGTCCCCAAA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCACATTTGTGACGCAAAATACCACCTTGGCGCCCTACACGGGAGACGAC 601
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

02210-2211

COMPUTER:

IBM Compatible

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alignment_block:
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352 CGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCA 401
                                                                                           302 CTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGAT 351
                                                                                                                                 105 AlaArgValArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSe 121
                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                        161
                                                 121 rSerAlaAspValAlaLeuValGluLeuGluAlaProValProPheThrA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 CCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATAC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGY: linear
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APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                    72 rAlaAlaHisCysPhe...ArgAsnThrSerGluThrSerLeuTyrGlnV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCCAGGCCAGGCCTGCAGCGAGTGGGCATCGTTGGGGGTCAGGAGGCCC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 aCysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CTGCTGCTGCCCCGTCCTGGCGAGCCGCGCCTACGCGGCCCTAC 60
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FORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LeuLeuLeuLeuCysPheGlySerGlnArgAlaLysAlaAlaThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                             alLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyr 104
                                                                                                                                                                                                                                                                                                                                                                    TGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGAC 210
                                                                                                                                                                                                                                                                                                                                                                                           ....SerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh 72
                                                                                                                                                                                   TGCAACTGCGGGAGCAGCACCTCTACTAC.....CAGGACCAGCTG 301
                                                                                                                                                                                                                                                                          CGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGG 260
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3.147
68.248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B0801/7090
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                   APPLICATION NUMBER: 60/037,090 FILING DATE: 05-FEB-1997 ATTORNEY/AGENT INFORMATION: NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                           CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 pileHisArgIleIleProLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           746 CAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                696 ATGCCACCTGCCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 lyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGluGlyCysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 GGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: 1
                                          NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b, Application US/09016366A
5955431
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                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                   Diskette
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alignment_block:
US-10-041-006-7 x US-09-016-366A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                    400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CGGAGCGGACATCGCCCTGCTGGAGCTGGAGGCCGGTGAACGTCTCCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 TGCAACTGCGGGAGCAGCACCTCTACTAC......CAGGACCAGCTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 TGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGAC
600 GTCCGCATCGTCCGTGACGACATGCTGTGCCGGG.....AACACCCG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AlaArgValArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00 CTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGAT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 lnGluGlyGluTrpProTrpGlnValSerIleGlnArgAsnGly.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 rAlaAlaHisCysPhe...ArgAsnThrSerGluThrSerLeuTyrGlnV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LeuLeuLeuLeuCysPheGlySerGlnArgAlaLysAlaAlaThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...SerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATAC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCAGGCCAGGCCCTGCAGCGAGTGGGCATCGTCGGGGGGTCAGGAGGCCC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aCysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTGCTGCCGCCTGCCGTCCTGGCGAGCCGCGCCCTACGCGGCCCCTGC
                            ProLysThrIleLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLy 221
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCACGTCCACACGGTCACCCTGCCCCCGCCTCAGAGACCTTCCCCCCG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyr 104
                                                                                                        ACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGAC 599
                                                                                                                                                     hrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGln 204
                                                                                                                                                                                                              CCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAA 549
                                                                                                                                                                                                                                                                                                                      GGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCG 499
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seq_documentation_block:
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                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-978-404B-13
Align seg 1/1 to: US-08-978-404B-13
                                                                       US-10-041-006-7 x US-08-978-404B-13
                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 1137 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Gre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 pIleHisArgIleIleProLys 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 sLysAspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuValG
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 600 P
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MAST CELL PROTEASE THAT CLEAVES
FIBRINGGEN
                                                                                                                                                                                          Percent Identity: 43.796
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to: 1137
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GATCCACCACTATGTCCCCAAA 815
                                       pIleHisArgIleIleProLys 278
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seq\_name: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:US-08-978-404B-1
seq\_documentation\_block:
; Sequence 1, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:

alignment\_scores:
Quality: alignment\_block: US-08-978-404B-1 Align seg 1/1 to: US-08-978-404B-1 from: 1 to: US-10-041-006-7 x US-08-978-404B-1 Percent Similarity: REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: BORG
TELECOMMUNICATION INFORMATION:
"PI.EPHONE: 617-720-3500 INFORMATION FOR SEQ ID NO: 280 GAGTACAGCTCCGTAAGCAGTACCTCTATTAC.....CATGACCAC 230 SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C. APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN 130 CACATGGGAACAAGTGGCCCTGGCAGGTGAGCCTGCGTGCCAATGACACC OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM 87 lnValLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMet 103 71 uThrAlaAlaHisCysPhe...ArgAsnThrSerGluThrSerLeuTyrG 41 hrGlnGluGlyGluTrpProTrpGlnValSerIleGlnArgAsnGlySer 57 89 T.....CCAGCTATGACACGAGAAGGCATTGTGGGGGGACAGGAGG 25 aCysGlyArgProArgMetLeuAsnArg...MetValGlyGlyGlnAspT : :::::: :::||||||||||||:::: 9 LeuLeuLeuLeuCysPheGlySerGlnArgAlaLysAlaAlaThrAl 25 STATE: N COUNTRY: APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOV-97 TOPOLOGY: TELEX: COMPUTER: CLASSIFICATION: MEDIUM TYPE: Diskette STREET: CACTGCGGCACACTGTGGGGACCGGATGTTGCTGACCCCAACAAGGTCA ......HisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLe 71 02210-2211 Boston Ratio: MA 600 Atlantic Avenue U.S.A. linear IBM Compatible 68.000 578.50 3.094 60/032,354 Percent Identity: 45.455 B0801/7090 Gaps: 1031 129 87 179 41 88 229

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Aence 22, Application US/09016366A

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 GCACAGCCCAACAGGCCTGGCATCTACACCCGGGTCACCTATTACTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668 A...CATGACTCCTGCCAGGGCGACTCCGGAGGACCTCTGGTCTGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 yLysLysAspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571
                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            815 CTGGATCCACCACTATGTCCCCAAG 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 nTrpIleHisArgIleIleProLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ame: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 AlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHisAs 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrAsnTyrIleLeuProValCysLeuProAspProSerValIlePheGlu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATGGGGCAGACATTGCCCTGCTGAAACTCACAAACCCTGTGAACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGTCCACATTGTCCGAGATGACATGCTGTGTGCTGGG...AATGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAACCACCTTTGTGACTTGAAGTATCACAAAGGTCTCATCACAGGTGAC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyr 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pLeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGGAACGTTGTGCTGGGTGACAGGCTGGGGTAACATCGACAATGGTGT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGluAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGACTATGTCCACCCTGTCCCCCTACCTCCTGCCTCAGAGACCTTCCCC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aSerSerAlaAspValAlaLeuValGluLeuGluAlaProValProPheT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrAlaArgValArgGlnValGluSerAsnProLeuTyrGlnGlyThrAl 120
                                                                                                                                                                                                                                                                    M
                                                                                                                                                                                                                                                                                                                   600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                               Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667
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US-09-016-366A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-016-366A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-041-006-7 x US-09-016-366A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                    305 CACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGGTGGA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TGAGCCTGAGAGTCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
                                             179 nLysLeuAlaValProIleIleAspThrProLysCysAsnLeuLeuTyrS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 CTCATCCACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGA 213
                                                                                                                                                                                                                                                                                                                                                    129 uLeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuValGl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 ACTAC.....CAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 CGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 alGlnProGlyProHisAlaMetTyrAlaArgValArgGlnValGluSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 nThrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LeuIleAlaGluGlnTrpValLeuThrAlaAlaHisCysPhe...ArgAs 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 alSerIleGln......ArgAsnGlySerHisPheCysGlyGlySer 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GGGCATCGTTGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 nArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnV::::||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GCGAGCCGCCTACGCGGCCCCTGCCCCAGGCCAGGCCCTGCAGCGAGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SerGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAs
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REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                             TrpGlySerProSerGluGluAspLeuLeuProGluProArgIleLeuGl 179
                                                                                                                                                                                                                                                                                                    GCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACC 554
                                                                                                                                                                                                     CCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGC
                                                                                                                                                                                                                                  roAspProSerValIlePheGluThrGlyMetAsnCysTrpValThrGly 162
                                                                                                  TGGGGCGATGTGGACAATGATGAGCGCCTCCCCACCGCCATTTCCTCTGAA
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3.179
68.421
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alignment_block:
                                                                                                     alignment_scores:
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                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08978404B Patent No. 5968782
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
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                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 IleArgValThrAlaHisHisAsnTrpIleHisArgIleIleProLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wolf, Greenfield & Sacks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 alIleSerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyValTyr 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             he: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-17
                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-720-2441
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyAspSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCGTGTCACCTACTAGTTGGACTGGATCCACCACTATGTCCCCCAAA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTAC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTGTGCCGGG.....AACACCCGGAGGGACTCATGCCAGGGCGACTC
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                                                                                                                                                                                                                              nucleic acid
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                                                                Ratio:
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                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                        578.50
3.179
68.421
                                                                                                                                                                                                          single
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                                           Percent Identity: 43.609
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seq_documentation_block:
; Sequence 15, Applicati
; Patent No. 6203979
                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-008-271A-15
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                                                                                                                                                                                                                                                                                                                                                                                     649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405
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                                                                                                                                                                                                                                                                            699 TGGTCAGCTGGGGCGAGGGCTGTGCCCAAGCCGAACCGGCCTGGCATCTAC
                                                                                                                                                                                                                                                                                                        246 alIleSerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyValTyr 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 ACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TrpGlySerProSerGluGluAspLeuLeuProGluProArgIleLeuGl 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 CACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 CGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCT
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                                                                                                                                                              749 ACCCGTGTCACCTACTTGGACTGGATCCACCACTATGTCCCCAAA 796
                                                                                                                                                                                                                   263 IleArgValThrAlaHisHisAsnTrpIleHisArgIleIleProLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 ACTAC.....CAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 CTCATCCACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LeuIleAlaGluGlnTrpValLeuThrAlaAlaHisCysPhe...ArgAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 alSerIleGln.....ArgAsnGlySerHisPheCysGlyGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 GGGCATCGTTGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GCGAGCCGCCTACGCGGCCCCTGCCCCAGGCCAGGCCCTGCAGCGAGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 SerGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                 rGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyAspSe
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                                                                                                                                                                                                                                                                                                                                                                                       CTGTGTGCCGGG.....AACACCCGGAGGGACTCATGCCAGGGCGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erLysAspThrGluPheGlyTyrGlnProLysThrIleLysAsnAspMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roAspProSerValIlePheGluThrGlyMetAsnCysTrpValThrGly 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uLeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nThrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAA 504
  5, Application US/09008271A
6203979
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GENERAL INFORMATION:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-041-006-7 x US-09-008-271A-15
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                          149 TCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGG 198
199 CCGTGGCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAG 248
                                                                                                                                        30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent_scores:
Quality:
                                         47 ProTrpGlnValSerIleGlnArgAsnGlySerHisPheCysGlyGlySe 63
                                                                                                                                                                                    99 GCCGGAGTCGCAGGAGGCGGCCCCTTATCAGGACCATGCGGCCGACGGG 148
                                                                                                                                                                                                                                                                               49 CGCGGGGCGCTGCTGCCTGCTGGCTCGGGCTGGACTCAGGAA
                                                                                                                                                                                                                                19 gAlaLysAlaAlaThrAla.....CysGlyArgProA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                           3 ArgProAlaAlaValProLeuLeuLeuLeuCysPheGlySerGlnAr 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/008,271A FILING DATE: 16-Jan-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
                                                                                                                                    rgMetLeuAsnArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrp 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: PROSTUT03
CLONE: 789927
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1081 base pairs
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Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue, Henry
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2.929
67.820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 42.561
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seq_documentation_block:
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                                                                          Sequence 4, Application US/09079970A
Patent No. 6274366
GENERAL INFORMATION:
APPLICANT: Maffitt, Mark A.
APPLICANT: Miles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 C...AAGGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 euLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAsp 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 AAACACATCCAGCCCATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 AsnTyrIleLeuProValCysLeuProAspProSerValIlePheGluTh 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAAT...T
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                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellect
                                                                                                                                                                                                                                                                                                                                                                                                                            878 GGATCCAGAAGCTGATG 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 ThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGl
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STREET:
E: Intellectual Property Department 8000 Excelsior Drive, Suite 401
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Madison

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alignment_block:
US-10-041-006-7 x US-09-079-970A-4
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
RECISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 3450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                    113 snProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuValGlu 129
                                                                                                                                                             166 GTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTA 215
                                                                                                                                                                                                                                           116 TCATCCACCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGAC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   64 euIleAlaGluGlnTrpValLeuThrAlaAlaHisCysPhe...ArgAsn 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (608) 831-2106
FORMATION FOR SEQ ID NO: 4:
EQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
                                                                                                                  96 lGlnProGlyProHisAlaMetTyrAlaArgValArgGlnValGluSerA 113
                                                                                                                                                                                                 80 ThrSerGluThrSerLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuVa 96
                                                                                                                                                                                                                                                                                                                            66 GAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCC 115
                                                                                                                                                                                                                                                                                                                                                                50 lSerIleGlnArgAsnGly......SerHisPheCysGlyGlySerL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                               34 ArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVa 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                             16 AGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCCTGGCAGGT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg 1/1 to: US-09-079-970A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WISCONSIN
ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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7..753
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7..18
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                                                                              .. CAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
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3.296
69.880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34506.073
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Steven:
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                 TELEPHONE: 617-720-3500
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stevens, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 leArgValThrAlaHisHisAsnTrpIleHisArgIleIleProLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 GGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 lIleSerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyValTyrI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 rLysAspThrGluPheGlyTyrGlnProLysThrIleLysAsnAspMetL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 rpGlySerProSerGluGluAspLeuLeuProGluProArgIleLeuGln 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701 CCCGTGTCACCTACTTGGACTGGATCCACCACTATGTCCCCAAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 LysLeuAlaValProIleIleAspThrProLysCysAsnLeuLeuTyrSe 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuPr 146
                                                           REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CONTROL OPERATING SYSTEM:
TELEFAX:
                                                                            NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 600 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGCGATGTGGACAATGATGAGCGCCCTCCCACCGCCATTTCCTCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              MΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 Atlantic Avenue
617-720-2441
                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richard L.
MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRINOGEN
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-978-404B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-978-404B-4 from: 1 to: 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-041-006-7 x US-08-978-404B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
216 yPheGluGluGlyLysLysAspAlaCysLysGlyAspSerGlyGlyProL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314
                                                                        611 TACACAGGAGATGATGTTCCCATTGTCCAGGATGGCATGCTGTGTGCTGG 660
                                                                                                                                                                                                                          183 alProIleIleAspThrProLysCysAsnLeuLeuTyrSerLysAspThr 199
                                                                                                                                                                                                                                                                                514 TAGTGACGAGCCTCTCCTGCCA...CCTTATCCTCTGAAGCAAGTGAAGG 560
                                                                                                                                                                                                                                                                                                              166 oSerGluGluAspLeuLeuProGluProArgIleLeuGlnLysLeuAlaV 183
                                                                                                                                                                                                                                                                                                                                                                                       464 ACCITCCCCTCGGGACTTCTTGCTGGGTAACAGGCTGGGGCGACATTGA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                  151 IlePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySer...Pr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 alProPheThrAsnTyrIleLeuProValCysLeuProAspProSerVal 150
                                                                                                                      200 GluPheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGl 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 TGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCTGCCTCGGAG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 Ala.....ArgValArgGlnValGluSerAsnProLeuTyrGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 TACAGCTTCGTGAGCAGTATCTA...........TACTAT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 TGGATGCATTTCTGTGGCGGCTCCCTCATTCACCCACAGTGGGTGCTCAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 CTGAAAGTAAGTGGCCCTGGCAGGTGAGCCTGAGATTTAAATTCAGCTTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 CACAGTCGAGGATGGGGCAGACATTGCCCTGCTGGAGCTTGAGATCCCTG 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 rAlaAlaHisCysPhe...ArgAsnThrSerGluThrSerLeuTyrGlnV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 .....HisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 aCysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrG 42 ::::::
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                            TCCCCATTGTGGAAAACAGCCTGTGTGATCGGAAGTACCACACTGGCCTC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGACCAGCTACTGACTGTGAACCGGACCGTTGTGCACCCCCCACTACTA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTTGCCCAGTCAAGCAGCGAGTGGGCATTGTGGGAGGACGAGAGGCTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTGCTGCTGGCACTGTCCCCCCTGGCTAGTCTGGTGCACGCGGC
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2.956
67.596
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alignment_block:
US-10-041-006-7 x US-09-016-366A-16
                                                                                                                               alignment_scores:
                                                                                                                                                                                                ; MOLECULE TYPE: US-09-016-366A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
; Sequence 16, Application US/09016366A
; Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-16
                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE 1154 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: U.S.A.
CIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chiiu TITLE OF INVENTION: MAST CELL. TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 CATCCAGGGTC 865
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OPERATING SYSTEM: DOS
SOFTWARE: FRANCES for Windows Version 2.0
                                                                                                                                                                                                                                                          TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                      TOPOLOGY:
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DEDNESS: single
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Align seg 1/1 to: US-09-016-366A-16 from: 1 to: 1154
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                                   271 pIleHisArgIleIleProLys 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GlySerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuTh 72
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GATCCACCACTATGTCCCCAAA 836
                                                                                                                                                                   ACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGAC 620
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9b_est2:BE590187

9b_est2:BI34059

9b_est2:BJ0704421

9b_htc:AK002694

9b_est1:AW765781

9b_est2:BI144993

9b_est2:BI902840

9b_est2:BG964050

9b_est2:BJ070867
                                                                                                                                                                                                          9b_est1:BB627930
9b_est1:AB627930
9b_est1:AL578261
1tc:AK006271
1tc:AK004239
est1:AL649451
9b_est1:BU25923336
9b_est2:BU259237
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Database: EST:*
Database sequences: 13736207
Database length: -1841457050
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gb_est1:AL555870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL-Frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US10041006/runat_13082002_083952_11232/app_query.fasta_1.350
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPELT=0.000 -LOOPEXT=0.000 -GGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPOXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPOXT=0.500 -DELOP=6.000
-DELEXT=7.000 -TATRT=1 -MATRIX=b1Dcsum62 -TRANS=humma140.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=-LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US1004106_@CGN1_1_2645
-CPU=5 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-XLPXY -WAIT -THREADS=1
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    1 Documentation
7 1 BG679626 607
                   9 i AKOJOGÓ MES MUSCULUS ES CELLS
1 ALS55870 ALS55870 LTI_NELOO6_PI
1 BB627930 BB627930 RIKEN full-le
1 BB627930 BB627930 RIKEN full-le
1 BG963117 602833094F1 NCI_CGAP_C
2 AL578261 AL578261 LTI_NELOO6_PI
2 AKOJOGO MES MUSCULUS adult ma
2 AKOJOGO MES MUSCULUS AGULT ma
3 AL649451 AL649451 XGC-gastrula
3 AL649451 AL649451 XGC-gastrula
4 AKOJOGO MES MUSCULUS AGULT ma
4 AKOJOGO MES MUSCULUS AGULT ma
4 BG97617 602833413F1 NCI_CGAP_C
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9 AKOJESO MUS MUSCULUS AGULT ma
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2 BI544641 603235988F1 NCI_CGAP_C
3 BI643250 602996390F1 NCI_CGAP_C
4 BAKOJOS546 MUS MUSCULUS AGULT fe
6 BE590187 197182 BARC 5BOV BOS T
8 BE590187 197182 BARC 5BOV BOS T
8 BUJ74421 BJ074421 NIBB MOChii r
1 BAKOJOS64 MUS MUSCULUS AGULT ma
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1 BUJ74421 BJ074421 NIBB MOChii r
1 BJ074491 BJ074421 NIBB MOChii r
1 BJ078840 BJ028840 NIBB MOChii r
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| AKO14645 Mus musculus 10 days
| AWI014645 Mus musculus 10 days
| AWI70323 xn59e12.xl Scares_NHCe
| AW084167 xc48c07.xl NCI_CGAP_E
| BB115142 BB115142 RIKEN full'-le
| BB1218460 602937954F1 NCI_CGAP_I
| BG962187 602836954F1 NCI_CGAP_I
| AL551470 AL551470 LTI_NELOO_PI
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gb_est2:BI771604
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gb_est2:BG966227
gb_est2:BG867549
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Quality: 1314.50
Ratio: 4.645
~'milarity: 93.709
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AUTHORS
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SOURCE
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                   34 rgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnVal 50
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                                                                                            rGlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnA 34
                                                                                                                                                                 MetArgArgProAlaAlaValProLeuLeuLeuLeuLeuCysPheGlySe
GAATGGTGGGCGGCAGGACACGCAGGAGGGGCGAGTGGCCCTGGCAAGTC
                                                                         TCAGAGGGCCAAGGCAACAGCCTGTGGTCGCCCCAGGATGCTGAACC
                                                                                                                                                ATGAGGCGGCGGCGGCGCTGCCTGCTGCTGCTGTTTTTGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Rogabs-remail.nih.gov

Email: ggabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10610 row: 1 column: 20
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947 bp mrNA linear EST 01-MAY-2001
602627678F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752547 5',
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High quality sequence stop: 865.
Location/Qualifiers
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National Institutes of Health, M
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/lab_host="DH10B (T1 phage-resistant)"
/note="organ: skin; Vector: pCMV-SPORR6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (
Average insert size 1.5kb. Library constructed by Lil
Technologies. Note: this is a NCI_CGAP Library."

1 298 c 308 g 154 t
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/db_xref="taxon:9606"
/clone="IMAGE:4752547"
/clone_lib="NCI_CGAP_Skn4"
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9 602786904F1 NCI_CGA
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LOCUS AK014645
                                                                         VERSION
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Mus musculus (strain:C57BL/6J) 10 days neonate skin cDNA to mRNA clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                    AK014645.1 GI:12852632
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                                                                                                             full insert sequence.
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CE 5 (bases 1 to 1323)

RRS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Oldo, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sonrimi, L., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, T., Shibata, Y., Tayama, M., Tagama, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GACAGAGARGCANCCAAKAGCTCTTTTTTTTTTTTTTTYN 3, CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 10.0.0. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashixo,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Quality:
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                                                                                                                                                                                                                                                                                 492 TTCTTGGAAGGAGGAACC.....CATGCAGACATTGCCCTGGTGCGCC 535
                                                                                                                                                                                                                                                                                                                                                                         442 CCAAGGTCCCAGAAAGTAGGCATTGCTTGGGTGCTGCCTCACCCCAGGTA 491
                                                                                                                                                                                                                                                                                                                                                                                                                     100 ProHisAlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuTy 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GGATTGTGGGAGGTGAGGACAGCATGGATGCCCAGTGGCCCTGGATTGTT
                                           163 pGlySerProSerGluGluAspLeuLeuProGluProArgIleLeuGlnL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 uGlnTrpValLeuThrAlaAlaHisCysPheArg...AsnThrSerGluT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AlaValProLeuLeuLeuLeuCysPheGlySerGlnArgAlaLysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGl 67
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                                                                                                                                      AspProSerValIlePheGluThrGlyMetAsnCysTrpValThrGlyTr 163
                                                                                                                                                                                                               euGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuPro 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCTGGGTGGTCACAGCCGCGCACTGCTTTAAGAGCAATATGGACAAAC 391
GGGAAGCATCCAGGATGGAGTGCCCCTGCCCCACCCTCAGACCCTTCAGA
                                                                                            GACTCCTCTCTCCCTCCCCAAGACCGACTGCTGGATTGCCGGCTG
                                                                                                                                                                                       TGGAACACTCCATCCAGTTCTCTGAGCGGATCCTGCCCATCTGCCTACCT 585
                                                                                                                                                                                                                                                                                                                          r.........GlnGlyThrAlaSerSerAlaAspValAlaLeuValGluL 130
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/clone_lib="RIKEN full-length
/dev_stage="10 days neonate"
1. .1323
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/db_xref="MGD:MGI:1903296"
/db_xref="taxon:10090"
/clone="4733401N09"
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/strain="C57BL/6J"
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1. .1323
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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCTCCTAGCTCACCGCTCCTGGGTGCAAAGGATCGTT 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xn59e12.x1 Soares_NHCeC_cervical_
IMAGE:2698030 3' similar to TR:08
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 602)
                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 452.
                                         adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                /lab_host="DH10B (phage-resistant)"
/note="Organ: cervix: Vector: pT7TDD-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5]
                                                                                                               T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clo
                                                                                                                                                           /clone="IMAGE:2698030"
/clone_lib="Soares_NHCeC_cervical_tumor"
/tissue_type="tumor"
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                   198 g
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Quality:

691.00

Length:

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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US-10-041-006-7 x AW170323/rev
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                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SION
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CE
RGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 TGCTGGGTCACGTGCTGCGGCAGCCCTAGTGAGTAAGACCTCCTGCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 CysTrpValThrGlyTrpGlySerProSerGluGluAspLeuLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgProGlyValTyrileArgValThrAlaHisHisAsnTrpIleHisAr 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCATCCCCAAACTGCAGTTCCAGCCAGCGAGGTTGGGCGGCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gIleI4eProLysLeuGlnPheGlnProAlaArgLeuGlyGlyGlnLys 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpLeuGlnAlaGlyValIleSerTrpGlyGluGlyCysAlaArgGlnAsn 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aCysLysGlyAspSerGlyGlyProLeuValCysLeuValGlyGlnSerT 241
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                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D.,
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencir
Clone distribution: NCI-CGAP clone distribution informatificund through the I.M.A.G.E. Consortium/LLNL at:
Possible reversed clone: polyT not
Seq primer: -40UP from Gibco
High quality sequence stop: 408.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW084167 MCI_CGAP_ESO2 Homo sapiens cDNA clone IMAGE:2587500 3' similar to TR:043342 O43342 SP001LA; mRNA sequence.
                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 601) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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AW084167.1 GI:6039319
                                                                                               www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
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96.241
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                                                                                                                                      information
                                                                                                                                                    Sequencing
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                                                                                                                                                                                                                                   Phillip
                                                                                                                                    ) Center
on can be
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VERSION
KEYWORDS
                                                                                                                                           seq_documentation_block:
LOCUS BB115142
                                       SOURCE
                                                                                                                                                                                           seq_name: gb_est1:BB115142
                                                                                        ACCESSION
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                       ORGANISM
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                                                                                                                                                                                                                                                                                                CATCGGATCATCCCCAAACTGCAAGTCCAACCCAGCGAGGTTGGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                   AGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCACCAACTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCCTGCAAGGGCGACTCGGCCGGCCCCCTGGTGTGCCTCGTGGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspAlaCysLysGlyAspSerGlyGlyProLeuValCysLeuValGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCA 452
                                                                                    625 bp mRNA linear EST 18-OCT-2001
BB115142 RIKEN full-length enriched, adult male urinary bladder Mus
musculus cDNA clone 9530049D14 3', mRNA sequence.
BB115142
                                                       EST
                   Mus musculus
                                                                      BB115142.2 GI:16261796
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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#: 11502-010"
157 c 203 g 127 t
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5.131
94.891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Eso2"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 27, 2000 this sequence version repla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., M., Koya, S., Watsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Division of Experimental Animal Research in Riken contributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse tissues
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second
                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="urinary bladder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="9530049D14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult male urinary
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AUTHORS
TITLE
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                                       JOURNAL
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seq_name: gb_est2:BI218460
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LOCUS BI218460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 alCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 roIleIleAspThrProLysCysAsnLeuLeuTyrSerLysAspThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 GluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAl 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 laArgLeuGlyGlyGlnLys 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGlyPh 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGTTGTGCCCGTCGGAATCGCCCAGGTGTCTACATCCGTGTGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCATTGACACGCCCAAGTGCAACCTGCTGTACAACAAAGATGTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                            GGAGAGCAGGCACCCAGCAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCCTTGTGGACCAGTCGTGGGTGCAGGCTGGGGGTGATCAGCTGGGGA
                                                                                                                                                                                                                                                               BIZ18460 889 bp mRNA linear EST 11-JUL-20 602937954F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5101213 5
                                                                                                                              Mus musculus
Unpublished (1999)
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                              mRNA sequence.
BI218460
                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                          nouse mouse
                                                                                                                                                                                                  BI218460.1 GI:14671904
                                                             (bases 1 to 889)
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4.897
93.571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
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                       Gene Collection (MGC)
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                                                                                           Mus.
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Strausberg, Ph.D

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alignment_block:
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171 LeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAs 187
                                                                                                  154 hrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGluAsp 170
                                                                                                                                                                                                             137 rAsnTyrIleLeuProValCysLeuProAspProSerValIlePheGluT 154
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                                                                                                                                                           354 TGACTACATGCTTCCAGTCTGCCTCCCGAAACCTGGCGACCCCCTGGATC 403
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                                                   CTGGCACCATGTGCTGGGTCACTGGCTGGGGACACATTGGCACAAATCAA 453
                                                                                                                                                                                                                                                                                               SerSerAlaAspValAlaLeuValGluLeuGluAlaProValProPheTh 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuThrAla 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTACCATCTCCTACCCTGAGGACAATGAGCCGAAGGAGCTGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCATTGCTTCAACCATGGCCAGTCCCTGTCTATCTACACAGTACTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGTGTGTGGACGTCCCAGGACATCAGGCCGCATCGTGTCAGGACAAGA 56
                                                                                                                                                                                                                                                                 AGCAGTGGAGACATTGCCCTGGTGCAGCTGGCTTCACCCATCTCCTTCAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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Plate: LLAM11243 row: 1 column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
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/Clone_lib="NCI_CGAP_L19"
/Clone_lib="NCI_CGAP_L19"
/lab_host="DBH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 249 c 242 g 210 t
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/strain="FVB/N"
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REFERENCE
AUTHORS
ORIGIN
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ORGANISM
                           BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 alGlyGlnSer.TrpLeu.GlnAlaGlyVallleSerTrpGlyGlu...G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 AAGAAGGATGCTTGTAAATGGTGATTCCGGAGGTCCCCTAGTCTGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 LysLysAspAlaCysLys.GlyAspSerGlyGlyProLeuValCysLeuV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 AGCCA...GTCATCCTTGAAGGCATGCTGTGTGCTGGTTTCCAGGAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 Tyrile 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 lyCysAlaArgGlnAsnArgPro.....GlyVal 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 TGCCGAGACCTGCAATACCTACTACCAGGAGAACTCCATTCCTGGCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGCATCTGTTCCAGAAGGCCACCGTGTTTACACCCCAACGGTCAGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Crar
Mammalia; Eutheria; Rodentia; Sciv
1 (bases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Man
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 675
                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BG962187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602826954F1 NCI_CGAP_Co24
                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAM10983 row: 1 column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG962187.1 GI:14349824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG962187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                           179
        //db_xref="taxon:10090"
//db_xref="taxon:10090"
//clone="TMAGE:4981789"
//clone=1b="NCI_CGAP_CO24"
//lab_host="DH10B (TI phage-resistant)"
//lab_host="DH10B (TI phage-resistant)"
//note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr
Site_2: SalI; Cloned unidirectionally by Life
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 213 c 234 g 176 t
                                                                                                                                                                                                                                                                  /strain="FVB/N"
                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 bp mRNA linear EST 12-JUN-2001 Mus musculus cDNA clone IMAGE:4981789 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650
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Quality:

591.50

Length:

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alignment_block:
US-10-041-006-7 x BG962187
                     seq_documentation_block:
LOCUS AL551470
  DEFINITION
                                                                             seq_name: gb_est1:AL551470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 CGCACGTGTGGGGGATCTCTGATTGCTGAGGACTGGGTGTTGACTGCT
                                                                                                                         723
                                                                                                                                                                                                                                                                                                                                                                                                             204 InProLysThrIleLysAsnAspMetLeuCysAlaGlyPheGluGluGly 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 CCGCTCCCAACAACCTTTACCCTGCAGGAGTTGCAGGTGCCTCTCATTGA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GGGTACCATCTCCTCCTACCCTGAGGACAATGAGCCGAAGGAGCTGAGAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 AlaHisCysPheArgAsnThrSerGluThrSerLeuTyrGlnValLeuLe 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erHisPheCysGlyGlySerLeuIleAlaGluGlnTrpValLeuThrAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGTGTGTGGACGTCCCAGGACATCAGGCCGCATCGTGTCAGGACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pThrGlnGluGlyGluTrpProTrpGlnValSerIleGlnArgAsnGlyS 57
                                                                                                                                                                                                                            ValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrpGlyGluGlyCy 253
                                                                                                                                                                                                                                                                                                           Lys.LysAspAlaCysLys.GlyAspSerGlyGlyProLeuValCysLeu 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACTACATGCTTCCAGTCTGCCTCCCGAAACCTGGCGACCCCCTGGATC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laArgValArgGlnValGluSerAsnProLeuTyrGlnGlyThrAla... 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCATTGCTTCAACCAGGGCCAGTCCCTGTCTATCTACACAGTACTGCT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCCAGCTGGGCCGTGGCCTTGGCAGGTCAGCGTGCGGGAGAATGGGG
                                                                                                                                                              sAlaArgGlnAsnArgProGlyValTyrIleArgValThr 266
                                                                                                                                                                                                                                                                                                                                                                     AGCCA...GTCATCCTTGAAGGCATGCTGTGTGCTGGTTTCCAGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCGAGACCTGCAATAACTACTACCAGGAGAACTCCATTCCTGGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAs 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAsnTyrIleLeuProValCysLeuProAspProSerValIlePheGluT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CT...GTGGCCCAGTTTATCAAGCACCCAAGCTATTCAGCGGACGAGCAC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uGlyAlaArgGlnLeuValGlnProGly.....ProHisAlaMetTyrA 105
                                                                                                                       TGCTCTGTACACAGACGCGGGGTGTTAACAGCAACGTCAGT 762
                                                                                                                                                                                                      ATAAATGATGTCTGGATCCAGGCAGGGAGTGGCGAGTGGGGATCTGATTG
                                                                                                                                                                                                                                                                                        AAGACAGGATGCTTGTAAATGGTGATTCCGGAGGTCCCCTAGTCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGTGGAGACATTGCCCTGGTGCAGCTGGCTTCACCCATCTCCTTCAA 375
AL551470 LTI_NFL006_PL2
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73.387
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Percent Identity: 49.597
  999
Homo
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bp mRNA
sapiens cD
RNA linear EST 16-FEB-2001 CDNA clone CS0DI064YF02 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
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AUTHORS
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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alignment_block:
US-10-041-006-7 x AL551470
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102 AlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuTyrGlnGl 118
                                                                                 359 CCTATGAGGTCAAGCTGGGGGCCCACCAGCTAGACTCCTACTCCGAGGAC 408
                                                                                                                                                                                                309 GTGGGTGCTGAGCTGCTCACTGCTTCCCCAGGGAGCACCACAAGGAAG
                                                                                                                                                                                                                                                                                                               259 ATCACCTATGAAGGCGTCCATGTGTGTGGTGGCTCTCTCGTGTCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                              209 TCACAGGTGGCAGCAGTGCAGTCGCCGGTCARTGGCCCTGGCAGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 GGAAGGGGCAGAAGCTCCCTGCGGTGTGGCCCCCCAAGCA.....CGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GCTGTGGCCATTCTGCTCTATCTTGGATTACTCCGGTCGGGGACAGGAGC 164
                                                                                                                                                                                                                                                                                                                                          52 IleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGluGl 68
                                                                                                               85 euTyrGlnValLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AlaValProLeuLeuLeu.....LeuLeuCysPheGlySerGlnAr
                                                                                                                                                                                                                                                      nTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluThrSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gAlaLysAlaAlaThrAlaCysGly...ArgProArgMetLeuAsnArgM 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prime, mRNA sequence. AL551470
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Genoscope · Centre National de Sequencage
BP 191 91006 EVRY cedex · France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
//tissue_type="placenta"
/note="Vector: pcWySPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcWySPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
190 a 331 c 295 g 190 t 4 others
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/clone_lib="LTI_NFL006_PL2"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKO10640 1629 bp mRNA linear HTC 19-JAN-MUS mUSCULUS ES cells cDNA, RIKEN full-length enriched library, Clone:2410039E18:Similar to PROSTASIN PRECURSOR (EC 3.4.21.-) (CHANNEL ACTIVATING PROTEASE 1), full insert sequence.
Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new of prepare full-length cDNA libraries.
                                                                                                                                                                        Carninoi, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (strain:C57BL/6J) ES cells cDNA to mRNA, clone_lib_RIKEN full-length enriched mouse cDNA libra
                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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similar to PROSTASIN PRECURSOR (EC 3.4.21.-) ACTIVATING PROTEASE 1)"
                                                        /note="data source:SPTR, source key:Q9ESD1, evidence:ISS
                                                                                           /clone_lib="RIKEN full-length enriched mouse cDNA library"
!. .1629
                                                                                                                                                                                   /clone="2410039E18"
                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                            /db_xref="MGD:MGI:1910128"
                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                cell_type="ES cells"
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                               (CHANNEL
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alignment_block:
US-10-041-006-7 x AK010640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AK010640 from: 1 to: 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
     838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 roValProPheThrAsnTyrIleLeuProValCysLeuProAspProSer 149
                                              233 euValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrp 249
                                                                                                                                                                                                                                                                                                                                                                               183 alProIleIleAspThrProLysCysAsnLeuLeuTyrSerLysAspThr 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::
492 CCGAGAAGAGGGCTCCCAGGGGGACATCGCGCTCATCCGCCTCAGCAGTC 541
                                                                                                          789 CTATGT.GAAGGGAGGCAAGATGCCTGCCAGGGTGACTCTGGGGGCCCAC
                                                                                                                                  216 yPheGluGluGlyLysLysAspAlaCysLysGlyAspSerGlyGlyProL 233
                                                                                                                                                                                                                                                                    200 GluPheGlyTyrGlnProLysThrIleLysAsnAspMetLeuCysAlaGl 216
                                                                                                                                                                                                                                                                                                                                                                                                                                         642 GGCTCCTTCAGTGAGCCTCCAGACCCCTAGGCCTCTGCAGCAGCTCGAGG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 oSerGluGluAspLeuLeuProGluProArgIleLeuGlnLysLeuAlaV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 GCCTCCTTTCCCAACGCCTTCACTGTACTGTCACGGGATGGGGTCATGT 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 ValilePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerPr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 rGlnGlyThrAlaSerSerAlaAspValAlaLeuValGluLeuGluAlaP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AATGACACTGTGGTCCACACAGTGGCTCAGATCATCACCCACTCAAGCTA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 GGGAAGCGTATGAGGTGAAGCTGGGGGCCCACCAGCTAGACTCCTACAGC 441
                                                                                                                                                                                                                                                                                                                              692 TACCACTCATCAGCCGGGAAACCTGTAGCTGCCTGTACAACATTAATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ProHisAlaMetTyrAlaArgValArgGlnValGluSerAsnProLeuTy 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TGACGGGACTGAAGCCTCCTGTGGTGCCGTCATCCAGCCA..... 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AAATAAATGGGTGGTGTCTGCTGCTCACTGCTTCCCCAGAGAACACAGCA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 ... CGCATCACCGGTGGTGGCAGTGCAAAGCCCGGTCAGTGGCCCTGGCAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GCTGTGACCATTCTGCTTCTTCGGATTGCTCCAGTCGGGAATCCGAGC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 hrSerLeuTyrGlnValLeuLeuGlyAlaArgGlnLeuValGlnProGly 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 aGluGlnTrpValLeuThrAlaAlaHisCysPheArgAsnThrSerGluT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 snArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGln 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 gAlaLysAlaAlaThrAlaCysGly.....ArgProArgMetLeuA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ValSerIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AlaValProLeuLeuLeuLeuCysPhe......GlySerGlnAr 19
TCTCTTGTCCCATGGAGGGCATCTGGTACTTGGCAGGCATTGTGAGTTGG
                                                                                                                                                                                                                     ... GTGCCTGAAGAACCGCACACTATCCAGCAGGACATGCTGTGTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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887
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est1:AL555870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AL555870
                                                                                                                                                                                                                                                                                                                                           US-10-041-006-7 x AL555870
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                         130 CATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         938 TACCTATGCTTCCTGGATCCACCACCATGTGGCAGAGCTCCAG 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 rAlaHisHisAsnTrpIleHisArgIleIleProLysLeuGln 280
180 GCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCAC
                            51 erIleGlnArgAsnGlySerHisPheCysGlyGlySerLeuIleAlaGlu
                                                                                                                                         34 gMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnValS 51
                                                                                                                                                                                          80 AGGCGGCGCGTGTATCAGGACCATGCGGCCGACGGGTCATCACGTCGCG
                                                                                                                                                                                                                                        18 GlnArgAlaLysAlaAlaThrAlaCysGlyArgProArgMetLeuAsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 876)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Ball 191006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: seqref@genoscope.cns.fr,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
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                                                                                                                                                                                                                                                                                                                                                                                                              573.00
3.032
70.522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWySpoRT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODX002YM07"
/clone="LTI_NFL006 PL2"
/tissue_type="placenta"
/note="vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 43.657
                                                                                                                                                                                                                                                                                        to: 876
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                                                                                           179
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seq_documentation_block:
LOCUS BB627930
                                                                         REFERENCE
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                                                                                                                                                                         SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 eIle 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        759 ATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATATCTATCTGAGCCCTCGCTACCTGGGGAAT...TCACCCTATGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCTGGGCACTCACGGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAGCT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGAATGGACTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                             gb_est1:BB627930
                                                                                                                                                                                                                                                                                                  BB627930 RIKEN full-length enriched,
1 (bases 1 to 626)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanag
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                           BB627930.1 GI:16465483
                                                                                                                                                                                                                                                                         musculus cDNA clone 9530049D14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                           mRNA
                                                  Furuno, M., Hanagaki, T., Hara, A.
                                                                                                                                                                                                                                                                                                  RNA linear EST 26-OCT-2001 adult male urinary bladder Mus
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                              Konno, H.,
                                                                                                                              Euteleostomi;
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COMMENT
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URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
Carninci.P., Shibata.Y., Muramatsu.M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
"S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sas, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details.
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                                                                                                                 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                     modified pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="urinary bladder"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="9530049D14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, adult male urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                             KS(+) after bulk excision
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                                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 728) 1 (bases 1 to 728) NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                         187 pThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrG 204
                                                                                           512 CCGCTCCCACCACCCTTTACCCTGCAGGAGTTGCAGGTGCCTCTCATTGA
                                                                                                                                                                                      462 CTGGCACCATGTGCTGGGTCACTGGCTGGGGACACATTGGCACAAATCAA
                                                                                                                                                                                                                 154 hrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGluAsp 170
                                                                                                                                                                                                                                                                                                                            137 rAsnTyrIleLeuProValCysLeuProAspProSerValIlePheGluT 154
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                                                                                                                      LeuLeuProGluProArgIleLeuGlnLySLeuAlaValProIleIleAs 187
                                                                                                                                                                                                                                                                                  TGACTACATGCTTCCAGTCTGCCTCCCGAAACCTGGCGACCCCCTGGATC
TGCCGAGACCTGCAATACCTACTACCAGGAGAACTCCATTCCTGGCACGG
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Plate: LLAM11003 row: 1 column:
High quality sequence stop: 728.
Location/Qualifiers
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/lab_host="DHIUB (TI phage-resistant)"
/lab_host="DHIUB (TI phage-resistant)"
/note="forgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 213 c 206 g 158 t
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4989478"
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                                      34 gMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnValS 51 | ::::|||||||||||| | |
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CATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCAGGGGA
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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/tissue_type="placenta"
/tissue_type="placenta"
/note="vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
/note="vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://filllosth.invitrogen.decom/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/library/sites/com/lib
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Location/Qualifiers
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/db_xref="taxon:9606"
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HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                         Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700023E12:protease, serine, 21, full insert
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                                 Submitted (10-JUL-2000) yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                      287 CAAAAGGATAACGATCCTTTTGACTGGACAGTCCAGTTTGGTGAGCTGAC 336
                                                                                                                             61 lyGlySerLeuIleAlaGluGlnTrpValLeuThrAlaAlaHisCysPhe 77
                                                                                                                                                                                                                                    44 yGluTrpProTrpGlnValSerIleGlnArgAsnGlySerHisPheCysG
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                                                            GCGCAACCTTGCTCAACCGCCGCTGGGTGCTTACAGCTGCCCACTGCTTC 286
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61.218
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
53. .943
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MsD:MGI:1901580"
/db_xref="taxon:10090"
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GRWPWQGSLRVWGNHLCGATLLNRRWVLTAAHCFQKDNDPFDWTVQFGELTSRPSLWN
LQAYSNRYQIEDIFLSPKYSEQYPNDIALLKLSSPVTYNNFIQPICLLNSTYKFENRT
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/protein_id="BAB24495.1"
/db_xref="GI:12839280"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 TTCCTGAGCCCCAAGTACTCGGAGCAGTATCCCCAAT...GACATAGCCCT
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3030 bp mRNA linear HTC 19-JAN-2002
Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300008A22:homolog to DJ1170K4.4 (NOVEL PROTEIN)
                                                                                                         Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                  Carninci, P.,
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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  Carninci,P., Shibata,Y.,
Itoh,M., Konno,H., Okazal
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ta,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Okazaki,Y., Muramatsu,M. and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUI-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URI:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kasukawa,T.,
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Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hamagaki, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RIKEN Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                             Host: SOLR.
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91. .2490
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                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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alignment_block:
US-10-041-006-7 x AK004939
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ORIGIN
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1856
polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                       107 alArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAla 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 heCysGlyGlySerLeuIleAlaGluGlnTrpValLeuThrAlaAlaHis 75 ::||||||||||:::||||||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 CysGlyArgProArgMetLeuAsnArgMetValGlyGlyGlnAspThrGl 42
                                                                                                                                                                                                                             AspValAlaLeuValGluLeuGluAlaProValProPheThrAsnTyrI1 140
|||||||||||||:::::|||::: ||||||| ::::::
GACGTGGCCCTGCTGCAGCTCGACCCCCGTGGTGTACTCGGCCACTGT 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAAGATGCGGCAGAACTCGCGCTGGCCAGGCGAGGTGTCCTTCAAGG
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                                                                                                                    GCGCCCCGTCTGCCTGCCCGCCTCCCACTTCTTTGAGCCAGGCCAGC 2155
                                                                                                                                                                          eLeuProValCysLeuProAspProSerValIlePheGluThrGlyMetA 157
                                                                                                                                                                                                                                                                                                                                                  TGAGCCGTCTGTTCCTGCACCCGTACCACGAGGAGGACAGCCATGACTAC 2055
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67.717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative"
903 c 883 g
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2373 CCGCTGGTTCCTGGCAGGGTTGGTTAGCTGGGGCCTGGGCTGTGGCCGAC 2422
2473 CAGCAGGTGCTG 2484
                                                                          2423 CCAATTTCTTTGGCGTCTACACCCGTGTCACACGTGTGATCAACTGGATC 2472
                                                                                                                                                                                                                                                                                                                                                                                      2250 CTGCAGTGAGGCCTACCGC...........TACCAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2200 GTGAGCAACACCCTGCAGAAGGTGGACGTACAGCTGGTCCCTCAGGACCT 2249
                                                                                                                                                                                                                            207 hrIleLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAsp 223
                                                                                               256 lnAsnArgProGlyValTyrIleArgValThrAlaHisHisAsnTrpIle 272
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                                                                                                                                                                          sCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysT 207
                                                                                                                                                                                                                                                                                                           2372
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